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G3P_ZYGRO
G3PZ_HUMAN
G3P1_JACOR
G3PZ_HUMAN
G3P1_GLORO
G3P_KLEPN
G3P1_GLORO
G3P_KLUILA
G3P1_ECOLI
G3PC_TRYBB
G3P2_YEAST
G3P2_YEAST
G3P2_AYBAN
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G3P2_DROME
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4 klebsiella
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kluyveromyc

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drosophila
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homo sapien
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 RESULT 1
G3P1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                          Glycolysis;
BINDING
ACT_SITE
       STRAND
TURN
                                       PRINTS; F
                                                                                                                                                                                                                                                                                                                                                           G3P1_HUMAN P00354;
                                                                  PDB; 3GPD; 1
MIM; 138400;
                                                                                PIR; A00366; DEHUG3
                                                                                                                                                                                                                Branowski T.;
                                                                                                                                                                                                                     Nowak K., Kuczek M.,
                                                                                                                                                                                                                            PARTIAL SEQUENCE. MEDLINE-76067491;
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                            [nterPro;
                                                    PF00044;
                                                                         16-JUL-88.
151
178
5
12
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151
178
8
12
23
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P34916 anabaena va	G3P1_ANAVA	ı	334	86.0	37	5
	G3P_STRAE	μ	333	86.0	37	4
Q92263 pichia past	G3P_PICPA	<u>, , , , , , , , , , , , , , , , , , , </u>	333	86.0	37	ω
	G3P_PALVE	μ.	333	86.0	37.	2
P00357 homarus ame	G3P_HOMAM	_	333	86.0	37	F
P29272 rhodobacter	G3P2_RHOSH	Н	333	86.0	37	5
P17721 thermotoga	G3P_THEMA	ب	332	86.0	37	39
Q59800 streptomyce	G3P_STRAU	ب	332	86.0	37	8
P26988 phytophthor	G3P_PHYIN	-	332	86.0	37	7
P55971 helicobacte	G3P_HELPY	سر	332	86.0	37	6
	G3P_HELPJ	ب	332	86.0	37.	5
Q01597 drosophila	G3P_DROHY	۳	332	86.0	37	34

## ALIGNMENTS

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X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

MEDLINE-76255083; pubMed=957435;

METCH NO. Winn S.I., Watson H.C.;

"Twinning in crystals of human skeletal muscle D-glyceraldehyde-3-phosphate dehydrogenase.";

J. Mol. Biol. 104:277-283(1976).

I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

I- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

I- SUBURIT: HOMOTETRAMER.

SUBURIT: HOMOTETRAMER.

GENERAL FOR THE SECOND PHASE OF GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-82073291; PubMed-7030790;
Nowak K., Wolny M., Banas T.;
"The complete amino acid sequence
phosphate dehydrogenase.";
PEBS Lett. 134:143-146(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from human muscles. Isolation and amino acid sequence from tryptic digest."; hoppe-Seyler's Z. Physiol. Chem. 356:1181-1183(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The covalent structure of glyceraldehyde-phosphate dehydrogenase
                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                 o; IPR000173; -.
F00044; gpdh; 1.
PR00078; G3PDHDRGNASE.
; PS00071; GAPDH; 1.
Oxidoreductase; NAD; Multigene family; 3D-structure.
151 151 GLYCERALDEHYDE 3-PHOSPHATE.
178 ACTIVATES THIOL GROUP DURING CATALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1193541;
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RESULT 2
G3P2_JACO
ID G3P2_J
AC P80447
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT GIYCER,
DE (FRAGM
GN GAPD O
OS JACULLU,
OC EUKARY,
OC EUKARY,
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Best Local S
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 TISSUB-Liver;
MEDLINE-96139342; PubMed-8547342;
Soukri A., Hafid N., Valverde F., Elkebbaj
"Evidence for a posttranslational covalent
glyceraldehyde-3-phosphate dehydrogenase in
                                                                                                                                                                                                          G3P2_JAGOR STANDARD; PRT; 25 AA.

P80447;
01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (EC 1.2.1.12) (GAPDH)
                                                                                        SEQUENCE.
                                                                                                                                     Jaculus
                                                                                                                                                                          (FRAGMENT).
GAPD OR GAPC.
Jaculus orientalis.
                                                                                                                  NCBI_TaxID=48868;
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rodentia;
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rde F., Elkebbaj M.S., Serrano ational covalent modification c dehydrogenase in hibernating j
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                                                                                                                                          Craniata; Vert
Sciurognathi;
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                                                                                                                                                        Vertebrata;
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Dipodidae; Dipodinae;
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RESULT 3
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Best Loc
Matches
                                                                                                          TISSUE=Lymphocytes;

Mertens B., Muriuki C.;

Submitted (JAN-197) to the EMBL/GenBank/DDBJ databases.

-1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDB 3-PHOSPHATE + ORT

+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

-1- PATHMAY: EIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-1- SUBUNIT: HOMOTETRAMER.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC.

-1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                  TISSUE-Liver;

MEDLINE-76087882; PubMed-1201027;

Kulbe K., Jackson K.W., Tang J.;

"Structural evidence for a liver-specific glyceraldehyde-3-phosphate dehydrogenase.";

dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              G3P_BOVIN
STANDARD; PRT; 320 AA.
P10096; P79130;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)
                                                                                                                                                                                                                                            SEQUENCE OF 10-320 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mammalia; Eutheria; Bovidae; Bovinae; Bc
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-30.
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                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Jaculus orientalis).";
Blochim. Biophys. Acta 1292:177-187(1996).
-: CAMALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
-: PATHWAY: FIRST STEP IN THE SCOND PHASE OF GLYCOLYSIS.
-: SUBUNIT: HOMOTETRAMER.
-: SUBCILLULAR LOCATION: CYTOPLASMIC.
-: PTM: THE HIBERNATING ADULT ISOFORM IS ADP-RIBOSYLATED. THIS ACCOUNTS FOR 2-3 FOLD LOWER SPECIFIC ACTIVITY IN THE HIBERNATING
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P; P00354; 3GPI
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GAPDH; ADP-ribosylation.

Feductase; NAD; ADP-ribosylation.

N -> D (IN HIBERNATIN
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2603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.4%;
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NON_TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence updat
15-JUL-1999 (Rel. 38, Last annotation upd
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
                                      Arnold H.H., Domdey H., Wiebauer K., I
"Cloning, partial sequencing, and expr
phosphate dehydrogenase gene in chick
J. Biol. Chem. 257:9872-9877(1982).
                                                                                                                TISSUE-Heart;
MEDLINE-82265644;
                                                                                                                                                                                                dehydrogenase
Proc. Natl. Ac
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    REVISION TO 328
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7; Conserv
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PIR; A00368; DECHG3.
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GLYCERALDEHYDE :
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differentially expressed in adult chickens but not chic
Nucleic Acids Res. 11:3301-3315(1983).
-i- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE +
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PATHWAY: FIRST STEP IN THE SECOND PHASE OF
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                                      2.1.12) (GAPDH).
                                                                                                                                                                                                                                                                                                                                       Length
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t chick embryos.
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RESULT 6
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Best Local
                dehydrogenase-encoding gene from quail embryo fibroblasts.";
Gene 128:269-272(1993), encoding quail embryo fibroblasts.";
-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
-I- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-I- SUBUNLT: HOMOTETRAMER.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                               MEDLINE=93292997; PubMed=8514192; Weiskirchen R., Siemeister G., Ha "Sequence and expression of a 9ly
                                                                                                                                      TISSUE-Fibroblast;
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                         Archosauria; Aves;
                                                                                                                                                                                                     Coturnix coturnix japonica (Japonica) (Japonica)
                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                      G3P_COTJA
Q05025;
                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRUDUTI; GAPDH; 1.

PROSITE; PS00071; GAPDH; 1.

Glycolysis; Oxidoreductase; NAD.

INT_MET 0 BY SIMILARITY.

BINDING 149 149 GLYCERALDEHYDE 3-PHOSPHATE.

176 176 ACTIVATES THIOL GROUP DURING CATALYSIS.
                                                                                                                                                                         NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF036934; AAB88869.1; -. InterPro; IPR000173; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a coetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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            SUBCELLULAR LOCATION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                         88.4%;
87.5%;
             THE
                                                                                                                                                                                                               (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB Pred. No. 6.3; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               ۳.
                                                                                             , Hartl M., Bister K.;
glyceraldehyde-3-phosphate
      GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                           332
                                                                                                                                                                                                                                                                                                                                                                                                       6.3;
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G3P_CRIGR
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Best Local S
Matches 7
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content endified and this statement is not removed. Usage by another entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           dehydrogenase mRNA.",
Nucleic Acids Res. 18:3054-3054(1990)
-!- CATALYTIC ACTIVITY: D-GLYCERALDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G3P_CRIGR
P17244;
O1-AUG-1990
O1-AUG-1990
15-JUL-1999
                                                                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                              Vincent S., Fort p.;
"Nucleotide sequence of hamster glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                          MEDLINE=90272420; PubMed=2349105;
                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster)
Eukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycolysis;
INIT_MET
BINDING
ACT_SITE
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000173; -. Pfam; PF00044; gpdh; 1. PRINTS; PR00078; G3PDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z19086; CAA79512.1;
PIR; S35726; S35726.
PIR; JN0678; JN0678.
HSSP; P00334; 3GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC SIMILARITY: BELONGS TO THE GLYCER
                                                                                                                                                                                    CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH, = 1,3-DIPHOSPHATEGLYCERATE + NADH, PATHWAX: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS. SUBUNIT: HOMOTETRAMER.
                                                                                                                                      DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VNGFGRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VDGFGRIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00071; GAPDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 38, Last annotation update)
TORE 3-PHOSPHATE DEHYDROGENASE (EC.1.2.1.12) (GAPDH).
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                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB Pred. No. 6.3; 1; Mismatches
                                                                                                                                           GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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5.3;
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Best Local S
Matches 7
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical accordance in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G3P_MOUSE
P16858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S10221; DEHYG.
HSSP; P00354; 3GPD.
InterPro; IPR000173
                                                                                                                                                                                                                                                                                                                                                                                                   2-induced transcript
Gene 91:185-191(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last seq
30-MAY-2000 (Rel. 39, Last ann
GLYCERALDEHYDE 3-PHOSPHATE DEH
                                                Glycolysis;
INIT_MET
                                                                                                                              MGD;
                                                                                                                                         EMBL; M32599; AAA37659.1; --
PIR; JT0553; DEMSG.
HSSP; P00354; 3GPD.
SWISS-2DPAGE; P16858; MOUSE.
                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycolysis; Oxidoreductase; NAD. INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPROU0173; -.
Pfam; PF00044; gpdh; 1.
PRINTS; PROU078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                           InterPro; IPR000173; -.
Pfam; PF00004; gpdh; G3PDHDRGNASE.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sabath D.E., Broome
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91007274; PubMed=2145197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPD.
                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                            Sabath D.E., Broome H.E., Prystowsky M.B.;
"Glyceraldehyde-3-phosphate dehydrogenase mRNA is a major interleukin
2-induced transcript in a cloned T-helper lymphocyte.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VDGFGRIG
                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH(+) - 1,3-DIPHOSPHATEGLYCERATE + NADH.
PATHWAY: PIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
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                                                                                                                                                                                                                                                                                                              DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNGFGRIG
                                                                                                                               MGI:95640; Gapd.
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7; Conserv
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              332
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176
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176
                                                                Oxidoreductase;
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DEHYDROGENASE (EC
                                                                NAD.
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            GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURIN
; 53123085BEACF65D CRC64;
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ACTIVATES THIOL GROUP DURIN
BE970C395FD824B1 CRC64;
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                         CATALYSIS
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RESULT
G3P_PIG
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Best Local :
sequences.
Submitted
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Enzymes and isoenzymes: structure, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G3P_PIG STANDARD; PRT; 332 AA. P00355; Q29546; P79299; P79317; O18816; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 01-YDROGENASE (ECCENTED CONTROL OF THE PROPERTY 
                                                                                                                                                                                          TISSUE-Skeletal muscle;
Davoli R., Zambonelli P., Fo
Submitted (DEC-1995) to the
                                                                                                                                                                                                                                                                                                         Foss
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-125 FROM N.A. TISSUE-Small intestine; Winteroe A.K., Fredholm M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=76087882; PubMed=1201027;
Kulbe K.D., Jackson K.W., Tang J.;
"Structural evidence for a liver-specific glyceraldehyde-3-phosphate dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=68399311; PubMed=4299800;
Harris J.I., Perham R.N.;
"Glyceraldehyde 3-phosphate dehyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAPD.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
                                                                                                                                                                                                                                                     SEQUENCE OF 298-332 FROM
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 14-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Winteroe A.K., Fredholm M.;
Submitted (JAN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bendjani R., Silversides D.W.;
"Sus scrofa glyceraldehyde-3-phosphate dehydrogenase,
sequences.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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       TO THE GLYCERALDEHYDE 3-PHOSPHATE
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ne EMBL/GenBank/DDBJ
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Pred.
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018816;
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databases.
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                                                              GLYCOLYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscle.";
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic
                                                                                                   ORTHOPHOSPHATE
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DEHYDROGENASE FAMILY.

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RESULT 10
G3P_RABIT
ID G_3P_RA
AC P46406
DT 01-NOV
DT 15-JUL
DE GLYCER
GN GAPD.
OS Oryctc
OC Eukary
OC Manmal
OX NCBI_T
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLI)
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                P46406;
01-NOV-1995;
01-NOV-1995
15-JUL-1999
                                                                                                                                                      Eukaryota;
Mammalia; E
      MEDLINE-96011658;
                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq.
15-JUL-1999 (Rel. 38, Last ann.
GLYCERALDEHYDE 3-PHOSPHATE DEH
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                               Oryctolagus
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CON
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EMBL; X94251; CAA63935.1; --
EMBL; V84883; AAA91804.1; --
EMBL; U82261; AAB40155.1; --
EMBL; 284063; CAB06323.1; --
PIR; A00367; DEPGG3
PIR; B12055; B12055;
HSSP; P00354; 3GPD.
HSSP; P00354; 3GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycolysis;
INIT_MET
BINDING
ACT_SITE
CONFLICT
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5 VNGFGRIG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO00173; --
Pfam: PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 87.17; Conservative
                                                                                                                       cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Lagomorpha; Leporidae; Oryctolagus.
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PubMed~7590291;
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                                                                                                                                                                                                                                                 sequence update)
annotation update)
DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCERALDEHYDE 3-PHOSPHATE.

ACTIVATES THIOL GROUP DURING CATALYSIS.

N -> D (IN REF. 1).

N -> D (IN REF. 1).

N -> D (IN REF. 1).

N -> NP (IN REF. 3).

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O -> H (IN REF. 3).

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O -> S (IN REF. 3).

O -> S (IN REF. 3).

O -> DS (IN REF. 3).
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Pred. No. 6.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                        332
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6.3;
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RESULT
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Best Local
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                       SEQUENCE FROM N.A.
MEDLINE-8521556; PubMed=2987824;
Fort P., Marty L., Piechaczyk M.,
                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
11-CT-2000 (Rel. 40, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH) (38
BFA-DEPENDENT ADP-RIBOSYLATION SUBSTRATE) (BARS-38).
   Fort P., Marty L., Piechaczyk M., el Sabrouty S.,
Jeanteur P., Blanchard J.M.;
"Various rat adult tissues express only one major
                                                                                                                                                                                           G3P_RAT
P04797; P09328;
                                                                                                                                                                                                                                                                                                                                                                   BINDING
ACT_SITE
SEQUENCE
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EMBL; V00884; CAA24253.1; --
HSSP; P00354; 3GPD.
InterPro; IPR000173; --
Pfam; PF00044; 9Pdh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to icense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                     Glycolysis;
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                            Local Similarity
nes 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putney S.D., Herilhy W.C., Schimmel P. "A new troponin T and CNA clones for found by shotgun sequencing.";
Nature 302:718-721(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the rabbit glyceraldehyde-3-phosphate dehydrogenase-gcoding cDNA.";
Gene 163:325-326(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 32-78 FROM N.A. MEDLINE=83167564; PubMed=6687628;
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5 VNGFGRIG 12
                                                                                                                                                                                                                                                                            1 VDGFGRIG 8
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Jaeck H.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  F00044; gpdh; 1.
PR00078; G3PDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                           PS00071; GAPDH;
                                                                                                                                                                                                                                                                                                                                                                   332 AA;
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OXIGOREGUCTASE; NAD.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                      STANDARD;
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176
. 35688 MW;
                                                                                                                                                                                                                                                                                                                    88.4%;
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OSPHATEGLYCERATE + NADH
                                                                                                                                                                                                                                                                                                     Score 38; DB Pred. No. 6.3; 1; Mismatches
                                                                                                                                                                                                                                                                                                        ۲;
                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                         GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING
; 14B5051B1722A19A CRC64;
                                                                                                                                                                                                    PRT;
only one major mRNA species
                                                                                                                                                                                                  332
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for 13;
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Plechaczyk M., Blanchard J.M., Marty L., Dani C., Panableres F.
el Sabrouty S., Fort P., Jeanteur P.;
"Post-transcriptional regulation of glyceraldehyde-3-phosphate;-
dehydrogenase gene expression in rat tissues.";
nucleic Acids Res. 12:6951-6963(1984).
                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Trifluoperazine activates and releases latent ATP-generating enzymes associated with the synaptic plasma membrane.";
J. Neurochem. 49:232-238(1987).
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                                                                                                                                                              InterPro; IPRO00173; -.
Pfam; PF00044; 9pdh; GJPDHDRGNASE.
PRINTS; PR00078; GJPDH; 1.
PROSITE; PS00071; GAPDH; 1.
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"1.5 kb mRNA abundantly expressed in
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Nucleic Acids Res. 13:1431-1442(1985):
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01-AUG-1988
15-JUL-1999
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13-AUG-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
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Homo sapiens (Human).
Eukaryota; Metazoa; C
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Glycolysis; Oxidoreductase; NAI
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
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-!- CATALYTIC ACTIVITY: D-GLYCERALDEH
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SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

EQUENCE FROM

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                                         SEQUENCE FROM N.A. Zhou J., Yu W., Ta Margolin J.F.;
                                                                                                                      Ye Z., Connor J.R., "cDNA cloning by amplification of circularized first reveals non-TRE-regulated iron-responsive mRNAs."; Biochem. Biophys. Res. Commun. 275:223-227(2000).
                       Submitted
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDILINE-87109159; PubMed=3027061;
Allen R.W., Trach K.A., Hoch J.A.;

"Identification of the 37-kDa protein displaying interaction with the erythroid cell membrane as 91yceraldehyde-3-phosphate dehydrogenase.";
J. Biol. Chem. 262:649-653(1987).
                                                                                                                                                                                                                           MEDLINE=20403900; PubMed=10944468;
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=88026722; PubMed=3664468;
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MEDLINE-92020872; PubMed-1924305;
Meyer-Siegler K., Mauro D.J., Seal G.,
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Arcarl P., Martinelli R., Salvatore F.;
"The complete sequence of a full length cDNA for human
glyceraldehyde-3-phosphate dehydrogenase: evidence for
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               (JUL-2000) to
                                                             W., Tang H.,
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EMBL/GenBank/DDBJ databases
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                                              Bouck J.,
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pseudogene; a
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G3PL_JACOR STANDARD; PRT; 363 AA.

AC P80534; 064418;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FCB (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, M(
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                                                                                                                                                                                                                                                                             Query Match
Best Local
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SWISS-2DPAGE; P04406; HUMAN.
Aarhus/Glent-2DPAGE; 1206; NE
HSC-2DPAGE; P04406; HUMAN.
MIN; 138400;
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PIR; 821939; 822939.
PIR; A21939; A21939.
PIR; A31988; A31988
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EMBL; V01677; CAA25833.1; --
EMBL; V04038; AAA53191.1; --
EMBL; X53778; CAA37794.1; --
EMBL; X53778; CAA37794.1; --
EMBL; M33197; AAA52818.1; --
EMBL; M32072; AAA52818.1; --
EMBL; AF261085; AAF59678.1; --
EMBL; AY007133; AA601996.1; --
EMBL; AY007133; AA601996.1; --
                                                                                                                                                                                                                                                                                      Glycolysis; (INIT_MET BINDING ACT_SITE CONFLICT
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00044;
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PIR; A45924;
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KOVALYOV L.I., Shishkin S.S., Efimochkin A.S., KoVALYOVA M.A.,

Ershova E.S., Egorov T.A., Musalyamov A.K.;

"The major protein expression profile and two-dimensional protein
database of human heart.";

CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE

-!- CATALYTIC ACTIVITY: D-GLYCERATE + NADH.

-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-!- SUBLULIAR LOCATION: CYTOPLASMIC.

-!- SUBCELLULAR LOCATION: OTHE GLYCERALDEHYDE 3-PHOSPHATE

-!- SUBCELLULAR LOCATION: OTHE GLYCERALDEHYDE 3-PHOSPHATE

-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by modified
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SEQUENCE OF 219-225 AND 241-245.
                                                                                                                                                VNGFGRIG
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                                                                                                                                                                                                   Similarity 87.
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                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Multigene family
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A41297.
A45924.
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Pred. No. 6.3;
1; Mismatches
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ACTIVATES THIOL GROUP DURING CATALYSIS.
N -> D (IN REF. 4).
; 6CE6C4ABAF54C377 CRC64;
                update)
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 (EC
1.2.1.12)
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Jaculus orientalis. Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Dipodidae; Dipodinae;

Jaculus.

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RESULT 15
G3P1_AA
AC P80506
DT 01-FEB
DT 15-JUL
DE GLYCER
DE (FRAGM
GN GAP1.
OS Anabae
OC NCB1_T
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Best Local S
Matches 7
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Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 1 (EC
                                                                                                       G3P1_ANASP
P80506;
                                                                                                                                                                                                                                                                                                                   PROSITE;
Glycolysi
                                                                                                                                                                                                                                                                                                                                                        EMBL; X87226; CAA60678.1;
HSSP; P00354; 3GPD.
InterPro; IPR000173; -.
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                                                                                                                                                                                                                                                                                                                            Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soukri A., Serrano A.;
Submitted (JAN-1996) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
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                                                   (FRAGMENT).
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(BY SIMILARITY).
ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
6CB549D9A1163C3F CRC64;
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                    Nostocaceae; Nostoc
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Query Match
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                                                                           Glycolysis; Oxidoreductase; NON_TER 35 35 SEQUENCE 35 AA; 3788 MW;
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VALVERDE F., SETTAND A.;
SUBMILTED (NOV-1995) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
                                                                                                  Interpro; IPR000173; -
PROSITE; PS00071; GAPDH; PARTIAL.
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Search completed: June 13, 2001, 14:30:38 Job time: 528 sec

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1: sp_archea:*
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sp_vertebrate:*
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Q9QWU4
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Q9M7R4
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097652
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Q9MZ05
Q9NZD6
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Opn205 felis silve
Opn205 felis silve
Opm7r7 odontella s
Opm7r7 odontella s
Opm7r7 phaeodactyl
Opm907 arabidopsis
Opm119 arabidopsis
Opm152 streptococc
P90514 acanthamoeb
O15558 trichomonas
O15559 trichomonas
O15559 trichomonas
O1977 kluyveromyc
Q41949 arabidopsis
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O52631 clostridium	Q9ptw5 paralichthy	Q9kt36 vibrio chol	Q9wwl7 synechococc	Q9x7h5 paracoccus			Q9pmq4 campylobact		Q9v318 drosophila	Q9kqj8 vibrio chol		Q915x6 streptococc	Q9wwl6 synechococc	Q9x6z1 burkholderi		<ul> <li>Q03596 salmonella</li> </ul>	Q03595 salmonella	Q03594 salmonella	Q56094 salmonella	$\sim$	0	rattus r	Q9sec3 lactuca sat	Q9spk8 lactuca sat	Q9y7h1 piromyces s

## ALIGNMENTS

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Best Local :
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097653;
097653;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (FRAGMENT)
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QVB1 PRELIMINARY; PRT; 29 AA.
Q9QVB1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NITRIC OXIDE-ENHANCED ADP-RIBOSYLATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate dehydrogenase.";
Proc. Natl. Acad. Sci. U.S.A. 89:9382-9385(1992).
INTERPRO; IPRO00173; -.
PFAM; PF00044; 9pdh; 1.
SEQUENCE 29 AA; 3109 MW; 5133EB197FC96EEA CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                  097653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93028468; PubMed-1409644;
Zhang J., Snyder S.H.;
"Nitric oxide stimulates auto-ADP-ribosylation of glyceraldehyde-3-
phosphate dehydrogenase.":
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5 VNGFGRIG
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P97617
ID P
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DT 0
DT 0
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GN GGN GGN R
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Best Local (
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO, IPRO00173; -. PFAM; PF00044; gpdh; 1. NON_TER 1 1 1 NON_TER 76 76 SEQUENCE 76 AA; 8334 MW; D
  P97617 PRELIMINARY; PRT; 83 AA.
P97617; PRT (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCETALDEHYDE 3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O97652

PRELIMINARY; PRT; 76 AA.
O97652;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
Fells silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leutenegger C.M., Mislin C., Lutz H.;
"Partial Characterization of feline glyceraldehyde-3-ph.dehydrogenase (GAPDH).";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF09717; AAC72840.1;
**TWWTEDEDC.** JGCD.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Leutenegger C.M., Mislin C., Akens M., von Rechenberg B.
"Partial characterization of equine glyceraldehyde-3-phc
dehydrogenase (AspbH).",
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF097178; AAC72841.1; -
HSSP; P00354; 3GPD.
                                                                                                                                                                                                                                                                                                                           1 VDGFGRIG 8
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9796;
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norvegicus (Rat)
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7; Conserv
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IPRO00173; -. 00044; gpdh; 1.
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87
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                            7.58;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D3F3E09146FF7936 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akens M., von Rechenberg B., Auer
equine glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                              Mismatches
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ne glyceraldehyde-3-phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 76;
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Best Local S
Matches 7
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Q9MZ05
ID Q9
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Q9N2D6;
Q1-CCT-2000 (TrEMBLrel. 15, Careated)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
GAPDH.

Canis familiaris (Dog),

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;

NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                   Q9MZ05 PRELIMINARY;
Q9MZ05;
01-OCT-2000 (TrEMBLTel. 15, C)
01-CCT-2000 (TrEMBLTel. 15, Li
01-CCT-2000 (TrEMBLTel. 15, Li
GLYCERALDEHYDE-3-PHOSPHATE DEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00044; gpdh; 1.
NOW TER 83
SEQUENCE 83 AA.
                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                 Submitted (MAY-2000) to the
                                                                                                                                                                                                                                                                                                "Detection of PrPc sheep.";
                                                                                                                                                                                                                                                                           EMBL; AF272837;
                                                                                                                                                                                                                                                                                                                                                       Ovis aries (Sheep). Chordata; Craniat Mammalia; Eutheria; Chordata; Craniat Mammalia; Eutheria; Cetartiodactyla; Bovidae; Caprinae; Ovis. NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                         Herrmann L.M.,
                                                                                                                                                                                                                                                                                                                   Knowles D.P.;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WISTAR-KYOTO; TISSUE-AORTIC SMOOTH MUSCLE; Adams L.A., Werny I., Schwartz S.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U75401; AAB19105.1; -. HSSP; P17721; 1HDG.
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                                                                                                                                                                       1 VDGFGRIG
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VDGFGRIG 8
|:||||||
6 VNGFGRIG 13
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                                                                                                                                                     VNGFGRIG 12
                                                                                                                                                                                          Similarity 87.57; Conservative
                                                                                                                                                                                                                                           106
106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 AA; 9240 MW;
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                                                                                                                                                                                                                                                                                                                        Davis W.C.,
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11612 MW;
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                                                                                                                                                                                                   88.4%;
87.5%;
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87
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                                                                                                                                                                                      Score 38; DB 6
Pred. No. 4.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                      Li H.,
                                                                                                                                                                                                                                                                                                                                                                                               , Created)
, Last sequence update)
, Last annotation update)
DEHYDROGENASE GAPDH (FRAGMENT).
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                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     B22E924D623D550A CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; [
Pred. No. 3.
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Sciurognathi; Muridae; Murinae; Rat
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3.5,
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                                                        update)
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      Euteleostom1;
Canis.
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10 N2D5
10 N2D
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Best Local S
Matches 7
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Best Loc
Matches
                                                                                                                                                                                                             Q9QWU4 PRELIMINARY; PRT; 333 AA.
Q9QWU4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitamura H., Adachi K., Kido N., Hagiya T., Minas
Yano E., Ohta Y., Tabu K., Mae J., Kanehira K., C
"Canine glyceraldehyde-3-phosphate dehydrogenase
CDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

TISSUE-WHITE ADIPOSE TISSUE;

Kitamura H., Adachi K., Ohta Y., Kido N., Hagiya T., Yasui H.,

Yano E., Minase K., Mae J., Tabu K., Kanehira K., Ohashi A.;

"Feline glyceraldehyde-3-phosphate dehydrogenase (GAPDH), compi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
NCBI_TaxID-9885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TremBLrel. 15, 01-0CT-2000 (TremBLrel. 15, 01-0CT-2000 (TremBLrel. 15, GLYCERALDEHYDE-3-PHOSPHATE)
  STRAIN-SPRAGUE-DAWLEY; Theng J., Ramirez V.D.; "Cloning of a rat brain
                                                                                                          Rattus norvegicus (Rat),
Eŭkaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AB038241; BAA90818.1; -. SEQUENCE 333 AA; 35813 MW; 20501C401BBE790
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SEQUENCE FROM N.A.
TISSUE-ADRENAL GLAND:
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9N2D5;
01-OCT-2000
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7; Conser
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BAA90817.1; -.
NA; 35861 MW; E08B4C39FA2AF7E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%;
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87
                                             TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .50
  glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Last sequence up, Last annotation DEHYDROGENASE.
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Pred.
                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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01-OCT-2000 (TrembLrel. 15, L
01-OCT-2000 (TrembLrel. 15, L
GLYCERALDEHYDE-3-PHOSPHATE DEI
GAPC1.
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Q9M7R7;
Q1-OCT-2000
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                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE PRECIDENCE.
                                                                                                                                                                                            Q9M7R4;
Q9M7R4;
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TRANSIT
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Liaud M.-F., Lichtle C., Apt K., Martin W., Cerff R.;
Liaud M.-F., Lichtle C., Apt K., Martin W., Cerff R.;
"Compartment-Specific Isoforms of TPI and GAPDH are Imported into Diatom Mitochondria as a Fusion Protein: Evidence in Favor of a Mitochondrial Origin of the Eukaryotic Glycolytic Pathway.";
Mol. Biol. Evol. 17:213-223(2000).
EMBL; AF063800; AAF34326.1; -.
                                                                                   Phaeodactylum tricornutum.
Eukaryota; stramenopiles; Bacilla
Bacillariophycidae; Naviculales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; stramenopiles; Biddulphiophycidae; Eupod: NCBI_TaxID=2839;
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SEQUENCE FROM N. Liaud M.-F., Lic
                                                              Bacillariophycidae;
NCBI_TaxID=2850;
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Submitted (NOV-1998) to the EN
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Eupodiscales; Eupodiscaceae;
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nlales; Phaeodactylaceae; Phaeodactylum.
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DEHYDROGENASE PRECURSOR.
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GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
; 73ADEF84E98FFC75 CRC64;
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Q1-MAY-1999 (TrEMBLrel. 1
Q1-MAY-1999 (TrEMBLrel. 1
Q1-MAY-2000 (TrEMBLrel. 1
E5Q4.8 PROTEIN.
                                  STRAIN-CV.
Rounsley S.
                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                            SEQUENCE FROM N.A
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujil C.Y., Utterback T.R., Barnstead
Roman C.L., White O., Nierman W.C., Fraser C.M.;
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F17A9 genomic seque
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC016827; AAF26996.1; -
SEQUENCE 871 AA; 98338 MW; 08ECE8F9297AD927 CRC64;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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EMBL; AF063803; AAF34329.1; ".
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379 AA;
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GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
, 913931B1E66EE302 CRC64;
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            Fujii C.Y.,
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Q9R5J2;
Q9R5J2;
Q1-MAY-2000 (TrEMBLrel. 1:
Q1-MAY-2000 (TrEMBLrel. 1:
Q1-OCT-2000 (TrEMBLrel. 1:
SURFACE DEHYDROGENASE (FR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 5
 J. Exp. Med. 176:415-426(1992).

HSSP; P00361; 1CER.

INTERPO, IPRO00173; -

PFAM; PF00044; gpdh; 1.
                                     activity."
J. Exp. Med
                                               Pancholi V., Fischetti V.A.;
"A major surface protein on group A strepglyceraldehyde-3-phosphate-dehydrogenase
                                                                                                                         Streptococcus.
Bacteria; Firmicutes;
                                                                                 MEDLINE-92364544;
                                                                                               SEQUENCE
                                                                                                                  NCBI_TaxID=1301;
                                                                                                                                                                                                                                                                                                                                           EMBL; AF1
NON_TER
SEQUENCE
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01-0CT-2000
01-0CT-2000
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Ch'ang L.Y., Lee T.;
Ch'ang D.Y., Lee T.;
"Trapping ORE-containing genomic
Submitted (DEC-1998) to the EMBL,
EMBL; AF110677; AAF66094.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NJT5;
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRAGMENT)
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00044; gpdh;
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(TrEMBLrel. 15, Last sequence update)
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(COSOMAL GLYCERALDEHYDE-3-PHOSPHATE DEHY
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                                                                                PubMed=1500854;
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                                                                                                                     Bacillus/Clostridium
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Last sequence update)
Last annotation update)
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Pred. No. 1.8;
2; Mismatches
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                     C9039F2CA020093A CRC64;
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ogenase with mu
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SEQUENCE 39 AA; 4284 MW; 911ED3AF6B50F66F CRC64;

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RESULT 15
P90514
ID P90514
AC P90514
AC P90514
AC P90514
CO O1-MAY
DT 01-MAY
DT 01-OCT
DE GLYCER
DE 3-PHOS
DE DEHYDR
OS ACANTH
OC Eukary
OX NCBI_T
RN (1)
RP SEQUEN
RA Xu P.
RL Submit
CC -1-CD
CC VI-CN
CC VI-CN
CC TITERE
DR HSSP,
DR INTERE
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DR INTERE
SQ SEQUEN
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Search completed: June 13, 2001, 14:29:46 Job time: 547 sec
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                                                                                                                                                                    Query Match 86.0
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                        Xu P., Zot H.G.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
L Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
2 -1 - CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOS
NAD(+) = 3-PHOSPHO-D- GLYCEROYL PHOSPHATE + NADH.
EMBL; U85500; AAB41646.1; -.
R EMBL; U85500; AAB41646.1; -.
R HSSP; OZ7890; IGYP.
R INTERPRO; IPR000173; -.
R PFAM; PF00044; 9pdh; 1.
W OX140reductase.
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P90514 PRELIMINARY; PRT; 49 AA.
p90514;
p90514;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
GLYCERALDEHYDE-3-PHOPHATE DEHYDROGENASE (EC 1.2.1.12) (GLYCERALDEHYDE
3-PHOSPHATE DEHYDROGENASE (PHOSPHORYLATING)) (TRIOSEPHOSPHATE
DEHYDROGENASE) (GAPDH) (FRACMENT).
ACANThamoeba castellanii (Amoeba).
EUKATYOta; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID-5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                     86.0%;
75.0%;
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Run on:

Title: Perfect score:

PCT-US01-05825A-30

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , 1 VDGFGRIG

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 13, 2001, 14:27:08; Search time 78.71 Seconds (without alignments) 1.953 Million cell updates/sec
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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 US-08-903-800A-6
5290690-9
US-07-928-462-2
US-08-273-247-2
US-08-637-759B-92
US-08-637-759B-92
US-08-637-35A-92
US-09-015-296-1
US-09-35-409-6
US-09-248-528-17
US-09-015-296-3
US-09-248-528-11
US-08-750-077-6
                                                                                                                                                                                                                        US-08-678-444-1
US-08-464-073-3-3
US-08-553-110-1
US-08-946-026-50
US-08-997-080-186
US-08-997-355-186
US-09-095-855-186
US-09-095-855-205
US-08-961-083-54
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Sequence 1, Appli
Sequence 3, Appl
Sequence 50, Appl
Sequence 186, App
Sequence 186, App
Sequence 186, App
Sequence 186, App
Sequence 204, Appli
Sequence 54, Appli
Sequence 54, Appli
Sequence 6, Appli
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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                                                                                                         US-08-678-444-1
                              Query Match
Best Local S
Matches 7
                                                                                                                                                          TELEFAX: (317) 276-3861
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08678444 Patent No. 5679349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Scheifinger, cu.
APPLICANT: Smiley, David L
TITLE OF INVENTION: VACCIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION UNMBER: 36,808
REFERENCE/DOCKET NUMBER: X-85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/678,444
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                      MOLECULE TYPE:
                                                                                                                             TYPE: amino ac STRANDEDNESS: TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Lilly Corp. CITY: Indianapolis STATE: Indiana
                                Local Similarity 87. 
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
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Lilly Corporate Center
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                                                                                                                                   SS: single
linear
                                                                                                                    peptide
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                                              97.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                               US/08/147,765
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US-08-464-523B-27

US-08-355-888A-7

US-08-588-190-2

US-08-588-526-2

US-08-693-697-7

US-08-640-389A-2

US-08-693-696-7

US-08-877-224B-9

US-08-440-845D-3

US-08-440-845D-3

US-08-440-845D-4

US-08-868-458-3

US-08-669-286-7

US-08-669-286-7

US-08-669-286-7
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                              Score 42; DB 1; Pred. No. 0.05; 1; Mismatches
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Result

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19

0

Minimum DB Maximum DB

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length: 0

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Database

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/
2: /cgn2\_6/ptodata/2/
2: /cgn2\_6/ptodata/2/
4: /cgn2\_6/ptodata/2/
5: /cgn2\_6/ptodata/2/
6: /cgn2\_6/ptodata/2/

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Sequence 1, Application US/08553110 Patent No. 5723301
                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                08-553-110-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                   CORRESPONDENCE ADDRESS:
                                                     APPLICANT: Strittmatter, Warren J.
TITLE OF INVENTION: Therapeutics for Diseases Associated
TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
NUMBER OF SEQUENCES: 2
                                                                                                          APPLICANT: Burke, James R. APPLICANT: Vance, Jeffrey M. APPLICANT: Enghild, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,058
FILING DATE: 03-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                      ADDRESSEE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                      Local Similarity 87.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           1 VDGFGRIG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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78'
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CANT: Sloud, Mouldy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Kenneth D. Sibley
D. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: PCT/AU/1993/00567
03-NOV-1993
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PROTEIN AND DEGRADATION RESISTANT MRNA DERIVATIVES
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TO NO.

ACTERISTICS:

18 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: per

US-08-553-110-1
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Best Local Similarity
""" 7; Conserve
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APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
AMAE: Maki, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/08946026 Patent No. 6034218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                         ZII: 98104-7092
ZII: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, St
APPLICANT: Dillon,
APPLICANT: Twardzik
APPLICANT: Mitcham,
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TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERICS:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                   STREET: 6300 Column
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/553,110 FILING DATE: CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            COUNTRY:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralass ""
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No. 5723301th Carolina
                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                     Twardzik, Daniel R.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Davin
                                                                                                                                                                                                                                                                                                                                                             AND IMMUNODIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
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                     210121.424C1
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Pred. No.
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                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity 87.5
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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ACTERISTICS:

ACT
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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                         VDGFGRIG 8
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VNGFGRIG 14
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                                                                                                                            Conservative
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linear
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87.5%;
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Pred. No. 4;
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Pred. No. 0.23;
                                                                                                                            Mismatches
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                           RESULT
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                                                                                                                                   Sequence 186, Application US/09095855
Patent No. 6160093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 186,
                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: U.S. Patent Application No. FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEAth, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                     APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                             7 VNGFGRIG
                                                                                                                                                                                                                                                                           1 VDGFGRIG 8
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                                                   Prestidge, Ross
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Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                               SS: single
linear
                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                             14
 Compounds and Methods for
Treatment and Diagnosis of Mycobacterial Infections
208
                                                                                                                                                                                                                                                                                                                             88.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186:
                                                                                                                                                                                                                                                                                                             Score 38; DB Pred. No. 4; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11000.1002c2
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                                                                                                                                                                                                                                                                                                                                               2
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ADDRESSEE:

USA

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Sequence 205, Application US/09095855 Patent No. 6160093
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FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                        TITLE OF INVENTED: 208

UNMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                       TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
                                                                                                                                                                                                                                                                                   APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
COMPUTER: IBM COMPT.

OPERATING SYSTEM: DOS

COFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARDE TO SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/095,855
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2601 Elliott Avenue, Suite 4185
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                                                                                        Diskette
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Pred. No. 4;
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                     RESULT 10
US-08-961-083-54
; Sequence 54, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
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FILING DATE: 30-APPLICATION UNIMBER: 728,833

FILING DATE: 30-APPLICATION UNIMBER: 728,833

FILING DATE: 30-APPLICATION UNIMBER: 728,833

FILING DATE: 30-APPLICATION UNIMBER: 6,710

FILING DATE: 30-DEC-1986

APPLICATION UNIMBER: 6,710

FILING DATE: 30-APPL-1985
                                                                                                                                                                                                                                                                                                                           5245013-20
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5245013-20
;Patent No. 5245013
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LENGTH: 27
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-205
                                                                                                                                                                                                                                  Query Match 86.0%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserv
            APPLICANT: Choi et. TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                   4 INGFGRIG 11
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APPLICATION NUMBER: US
                                                                                                                                                                                                   1 VDGFGRIG 8
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 Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                 Score 37; I
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0.55;
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Gaps

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US-09-095-855-205

COUNTRY: UZIP: 98121 STREET: 2601 E CITY: Seattle STATE: WA

WA USA

Gaps

0;

MEDIUM TYPE:

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VDGFGRIG 8

US-09-095-855-186

STRANDEDNESS:

TELEFAX:

FILING DATE:

Query Match Best Local S Matches 7

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

452

ADDRESSEE: STREET: 9

9410 Key West Avenue Human

Genome Sciences, Inc

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RESULT 12
5290690-11
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5290690-10. 5290690
PATENT NO. 5290690
PATENT RAPPLICANT: MRABET, NADIR; LASTERS, IGNACE; STANSSENS, PATRICK
MATTHYSSENS, GASTON; WODAK, SHOSHANA; QUAX, WILHELMUS J.
TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE
STABILITY OF PROTEINS
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-54
                                                                                                                                                                                                        5290690-10
                                                                                                                                                                                                                  ; FILING DATE: 25-AUG-1989;
SEQ ID NO:10:
LENGTH: 334
                                                                                                  Query Match
Best Local Similarity /J...
Best Local Similarity /J...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
COUNTRY: USA
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PB340P2
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                                                                                                                                        Score 37; DB 6; Pred. No. 7.9;
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Pred. No. 7.9;
                                                                                                                         Mismatches
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                                                                                                                                                       Length 334;
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US-08-903-800A-6
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APPLICANT: MRABET, NADIR;LASTERS, IGNACE;STANSSENS, PATRIC,MATTHYSSENS, GASTON;MODAK, SHOSHANA;QUAX, WILHELMUS J.

TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE
;STABILITY OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5935789
GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/398,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: RHEE, Sang-Ki
STREET: Keukdong Villa Ka-101, Kwangjang-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: AUTONOMOUSLY REPLICATING SEQUENCES, TITLE OF INVENTION: GAPDH GENE AND PROMOTER DERIVED FROM TITLE OF INVENTION: HANSENULA POLYMORPHA, EXPRESSION TITLE OF INVENTION: VECTORS CONTAINING SAME AND METHOD FOR TITLE OF INVENTION: THE SELECTION OF TRANSFORMANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CHOI, Eui-Sung
STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
STREET: Yuseong-gu
                                                                                                                                                                                                           COUNTRY: Republic of Korea ZIP: 302-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Daejeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                    STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong.
STREET: Seo-gu
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                 ADDRESSEE: KANG, Hyun-Ah
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6 INGFGRIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shindonga Apt.
                                                                                                                                                                                                                                                                                                                                                     E: SOHN, Jung-Hoon
Nuri Apt. 103-506,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHEE, Sang-Ki
CHOI, Eui-Sung
KIM, Chul-Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOHN, Jung-Hoon
KANG, Hyun-Ah
KIM, Hwa-Young
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Republic of Korea
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75.0%;
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Pred. No.
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STREET: #3-4 CITY: Seoul

#3-462,

Hwa-Young Bukahyun-3-dong, Seodaemun-gu

Republic of Korea

ADDRESSEE:

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5290690-9
1290690-9
1PATENT NO. 5290690
MATTHYSSENS, GASTON, WODAK, SHOSHANA; QUAX, WILHELMUS J.
TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE
1STABILITY OF PROTEINS
1STABILITY OF PROTEINS
                                                                                                                          5290690-9
                                                                                                                                   SEQ ID NO:9:
LENGTH: 335
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                                               Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 335 amino acid
                                                                                                                                                             NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/398,706
FILING DATE: 25-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 97-3173
FILING DATE: 31-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                    1 VDGFGRIG 8
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OTHER INFORMATION:
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                                                             86.0%;
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75.0%;
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dehydrogenase of Hansenula polymorpha
DL-1(ATCC 26012)
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                                            Score 37; DB Pred. No. 7.9; 2; Mismatches
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Pred. No. 7.9;
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                                                                         DB 6;
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                                                                    Length 335;
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Search completed: June 13, 2001, 14:27:09 Job time: 630 sec

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Best Local Similarity
""" 6; Conserv:
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US-07-928-462-2
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928.462
FILING DATE: 19920810
CLASSIFICATION E1
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/524.411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION TOMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik Data:
Saliwanchik Data:
                                                                                                                                                                                                                                         TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        NAME: Salivanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF, TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors
TITLE OF INVENTION: Fibrinolytic Agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              TOPOLOGY:
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7 INGFGRIG 14
                                 1 VDGFGRIG 8
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2421 N.W. 41st Street, Suite
                                                                   Conservative
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75.08;
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7.9;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length:
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1: /SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

6: /SIDS6/gcgdata/geneseq/geneseqp/AA1986.DAT:*

7: /SIDS6/gcgdata/geneseq/geneseqp/AA1986.DAT:*

8: /SIDS6/gcgdata/geneseq/geneseqp/AA1986.DAT:*

9: /SIDS6/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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Gapop 10.0 , Gapext 0.5
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B44447
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Human lung tumour-
Human lung tumour-
Breast cancer asso
Human HCMV inducib
Zea mays protein f
Zea mays protein f
Arabidopsis thalia
Lentinus edodes gl
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Human lung tumour
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Matches 19
The present invention describes lung tumour specific polynucleotides and tumour antigens. 207144 to 207246 and 208301 to 208325 represent specifically claimed polynucleotides, and Y29486 to Y29571 represent amino acid sequences from the present invention. The lung tumour
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28-JAN-1998,
28-JAN-1998,
18-MAR-1998,
18-MAR-1998,
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N-PSDB; Z07223.
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detection; inhibition.
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he blood-brain
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                    The present sequence is given in a specification relating to compounds for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer, especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                        Sequence
                                                                                                                                                            especially lung cancer
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09-AUG-1999;
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03-MAR-2000;
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N-PSDB; C79104.
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monitoring or treating
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28-JAN-1998;
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18-MAR-1998;
18-MAR-1998;
23-JUL-1998;
23-JUL-1998;
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   05-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09938973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lung tumour protein; therapy; diagnosis;
immunotherapy; detection; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lung tumour protein £86S-51 predicted amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y29540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunotherapy;
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                                                                                                                                                                                GLVLVGVNGFGRIGRI 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TN,
                                                                                                                                                                                                                                                                                                                            127 AA;
                                                                                                                                                                                                                                    Conservative
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes
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98US-0015022.
98US-0015029.
98US-0040828.
98US-0040831.
98US-0122191.
98US-0122192.
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                                                                    Protein; 127
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                                                                                                                                                                                                                                                   63.5%;
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                                                                                                                                                                                                                                                   Score 66; I
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                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                   DB 20;
0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibiting the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SG
                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung
                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                                                 0;
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Y07036
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Best Local S
Matches 13
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09-AUG-1999;
30-DEC-1999;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is given in a specification relating to compounds for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer, especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed
                                                                                                                                                                             Cancer associated breast cancer; col
                                                                                                                                                                                                                                                                                                         Y07036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lung tumor polypeptides and polynucleotides, useful for detecting, monitoring or treating cancer, especially lung cancer
                15-JUL-1998;
                                                    28-JAN-1999.
                                                                                       WO9904265-A2
                                                                                                                       Homo sapiens
                                                                                                                                                            prostate cancer.
                                                                                                                                                                                                                               Breast cancer associated antigen precursor sequence.
                                                                                                                                                                                                                                                                  02-JUL-1999
                                                                                                                                                                                                                                                                                                                                         Y07036 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2000; 2000WO-US08560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung tumour protein; lung cancer; cytostatic; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lung tumour-specific antigen encoded by cDNA #58
                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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DB; C79105.
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                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity 81.
13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0285323.
99US-0370838.
99US-0476235.
2000US-0518809.
                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                               colon
                  98WO-US14679
                                                                                                                                                                                                                                                                                                                                           Protein; 335
                                                                                                                                                                         antigen; diagnosis;
lon cancer; gastric (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  35
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1; Mismatches
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                                                                                                                                                                             cancer;
                                                                                                                                                                               research; treatment;
cancer; renal cancer;
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Length 127; Indels

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Gaps

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lung human;

cancer;

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RESULT
Y05368
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Best Local :
        22-SEP-1997;
08-SEP-1997;
                                           08-SEP-1998;
                                                                   18-MAR-1999
                                                                                        WO9913075-A2
                                                                                                                                   HCMV inducible gene, cig; human; human cytomegalovirus; interferon; anti-viral therapy; anti-HCMV therapy; detection; diagnosis;
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a binds to the NAM an expression product or a fragment of an expression product complexed with an expression product or a fragment of an expression interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast lung rancer. Colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                              Human HCMV inducible gene
                                                                                                                                                                                                         30-JUN-1999
                                                                                                                                                                                                                               Y05368;
                                                                                                                                                                                                                                                   Y05368 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 421-422; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tureci 0;
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|gkvkvgvngfgrigr1 17
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                                                                                                                                                                                                                                                                                                                                                                                                                  335
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                    (first entry)
       97US-0059725
97US-0058180
                                       98WO-US18638
                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
                                                                                                                                                                                                                                                   Protein; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Gure A,
Sahin U,
                                                                                                                                                                                                                                                                                                                                                                  63.5%;
                                                                                                                                                                           protein, SEQ ID NO 4.
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Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                  Score 66; I
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
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t E;
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RESULT
G54490
ID G5
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Best Local·S
Matches 13
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                                                                                                                                                                                              01-APR-1999;
06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                   23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                            09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999;
05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G54490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a human gene of the invention, and is induced to express by both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The invention also relates to genes that are repressed in the presence of HCMV infection, designated HCMV-repressible genes (crg or crgs). The products can be used to obtain agents which can be used for anti-viral therapy, particularly anti-HCMV therapy. They can also be used for the development of drugs that would allow for higher dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       termination sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes
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N-PSDB; X33938.
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nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 AA;
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                      99US-0123180
99US-0123548
99US-0125788
99US-0126264
99US-0126785
99US-0127462
99US-0128714
99US-0128714
99US-0128714
99US-013047
99US-0130449
99US-0130449
99US-0130449
99US-0131449
99US-0131449
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S-0132048.
S-0132407.
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Pred. No.
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0.05;
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				metabolic pathway; control; promoter;	·	136; .s 0; Gaps 0;	
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Best Local Similarity 62.0
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                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0161920.
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28-OCT-1999;
29-OCT-1999;
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N-PSDB; Al3531.
         Ubiquitin-ribosomal 40S protein
                            10-MAR-1998 (first entry)
                                                               W22503 standard; Protein; 338 AA.
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                   The present sequence represents glyceraldehyde 3 phosphate dehydrogenase (GPD) isolated from Lentinus edodes (Lentinula edodes; Camonly known as the shittake mushroom). The present invention describes the promoter and terminator regions from the promoter and terminator regions.
                                                                                                                                                                                                                                                                Disclosure; Page 14-15; 20pp; Japanese.
                                                                                                                                                                                                                                                                                  A promoter gene - comprising DNA selected from 1070 base pair sequence
                                                                                                                                                                                                                                                                                                                                                01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1998;
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                                                                                                                                                                                                           GDP gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter;
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99US-0162142.
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                                                                                                                                                     Score 63;
Pred. No.
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                                                     Human; prostate cancer; immunotherapy;
diagnosis; vaccine; antibody; human.
                                                                               Human prostate associated peptide
         Misc-difference
                                                                                                 27-APR-1998
                                                                                                                                    W27314 standard; Peptide; 18
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 46; 118pp; English.
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22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09723633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phaffia rhodozyma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KONN ) GIST-BROCADES BV.
                                                                                                                                                      13
                                                                                                                                                                               4 VLVGVNGFGRIGRI
| ||:||||||||
| 1 kvgingfgrigri
                                                                                                                                                                                                                   l Similarity 85. 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T72955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wery J;
                                                                                                (first entry)
                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96EP-0200943.
95EP-0203620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-EP05887
/note= "residue 1 may be any amino acid"
                  Location/Qualifiers
                                                                                                                                                                                                  17
                                                                                                                                                                                 16
                                                                                                                                                                                                                              60.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant DNA; astaxanthin; ribosomal protein;
                                                                                                                                    A
                                                                                                                                                                                                                            Score 63; DB 1
Pred. No. 0.14;
                                                                                                                                                                                                                    Mismatches
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The present sequence represents a ubiquitin-ribosomal 40S protein derived from Phaffla, which is mentioned in the disclosure of the present invention describing novel recombinant DNA. The recombinant DNA comprises a transcription promoter operably linked to a downstream sequence to be expressed, where the transcription promoter comprises a region found upstream of the open reading frame (ORF) of a highly expressed Phaffla gene (preferably GAPDH, a ribosomal protein gene, an enzyme involved in the biosynthesis pathway). The recombinant DNA can be used to transform hosts, preferably Phaffla. These transformed hosts are then used in the recombinant production of GAPDH or an enzyme involved in carotenoid synthesis, preferably astaxanthin. They may also be used to produce a pharmaceutical product. Purified carotenoids can be used as colourants in food and/or feed, and also in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phaffia derived GAPDH and carotenoid synthesis genes and promoter fragment - used in the recombinant production of therapeutically useful proteins e.g. carotenoids for use in food colouring
therapy; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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RESULT
W45521
ID W4:521
XX W4:
XX W4:
XX Q1
DT 27
XX G1
XX G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc human prostate prostate adenocarcinoma cell line LnCap.fgc (ATCC CRL 1740) with human prostatitis sera. Comparison of the peptide sequences with database sequences revealed homology to polypeptides not previously associated with human prostate. These were glyceraldehyde-3-phosphatate dehydrogenase (see W27316), calreticulin (see W27318 and W27319), malate dehydrogenase (see W27316), calreticulin (see W27318 and W27319), malate dehydrogenase (see W27313). Immunogenic portions of these peptides can be used in a claimed vaccine for treatment of prostate cancer, in a claimed vaccine for treatment of prostate cancer, in a claimed vaccine for treatment of prostate cancer, in for detecting prostate cancer or monitoring the progress of prostate cancer. 17 HPA polypeptides (see W27312-23 and W27303-07) and 14 other immunogenic polypeptides (see W27312-23 and W27303-07)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                          03-NOV-1995;
                                                                              03-MAR-1998.
                                                                                                                                  US5723301-A.
                                                                                                                                                                                                                                                                       Glyceraldehyde-3-phosphate dehydrogenase; GAPDH; polyglutamine;
                                                                                                                                                                                                                                                                                                                              Glyceraldehyde-3-phosphate dehydrogenase N-terminal sequence
                                                                                                                                                                                                                                          Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W45521 standard; peptide; 18
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W45521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 72; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 Peptides (W27314 and W27315) were obtained following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic portions of prostate proteins - useful to develop products to detect, monitor, treat or inhibit development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-1996;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VLVGVNGFGRIGRI 17
| ||||||||||
| 3 vkvgvngfgrigrl 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 85. 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                        omain; neurodegenerative disorder; inhibition; disease; schizophrenia; psychiatric disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                    95US-0553110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0633840.
96US-0616745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US04192
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85.7%;
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Pred. No. 0.009;
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RESULT
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Best Local S
The present sequence represents the N-terminal of a
                        Claim 12; Page 88; 106pp; English.
                                            New isolated prostate polypeptides useful diagnosis and monitoring of prostate cance
                                                                                                          Dillon DC,
                                                                                                                                                       23-JUN-1998;
07-OCT-1997;
                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                        07-OCT-1998;
                                                                                                                                                                                                                                                                      N-terminal; prostate tumour cell; immunogenic; treatment; prostate cancer; glyceraldehyde-3-phosphate dehydrogenase.
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                         Fragment of glyceraldehyde-3-phosphate dehydrogenase.
                                                                                                                                                                                                               15-APR-1999
                                                                                                                                                                                                                                     WO9918210-A2
                                                                                                                                                                                                                                                                                                                                        13-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                Y02457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the N-terminal sequence of glyceraldehyde-3-phosphate dehydrogenase (GAPDH). The invention relates to a new screening assay for compounds capable of inhibiting binding of GAPDH to polyglutamine. Compound, polyglutamine-containing an aqueous solution containing a test if binding of GAPDH to the polyglutamine-containing molecules and GAPDH and determining in the presence of the test compound. Inhibitors identified by the above assay could be used to treat neurodegenerative diseases or psychiatric disorders caused by a gene containing an extended CAG domain, e.g.
                                                                                                                                                                                                                                                                                                                                                                                Y02457 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 12; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening assay for inhibitors of GAPDH binding to poly:glutamine -for use in treating neuro-degenerative diseases or psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-178475/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VLVGVNGFGRIGRI 17
| ||||||||||
| 1 vkvgvngfgrigrl 14
                                                                                 1999-277272/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 85.7
                                                                                                       Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enghild J,
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                     98US-0102679
97US-0946026
                                                                                                                                                                                     98WO-US21166.
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                                                                                                        Reed
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                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                       SG,
                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; [Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                      Twardzik DR;
                                               cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                       the treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
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human

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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   Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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   protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June 13, 2001, 14:23:13 ; Search time 87.97 Seconds (without alignments)
17.187 Million cell updates/sec
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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104
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Compugen Ltd
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           glyceraldehyde-3-p
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58.7	58.7	58.7 58.7	58.7	58.7	59.1	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6
337	336	3 3 5 5	333	34	338	360	338	337	337	336	336	331	331	34
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DEUSGM	T40235	T40292	JC6310	A60475	JQ1287	S38570	JN0452	S29814	S26975	A42963	S71350	DEUTGC	DEECG3	A12055
glyceraldehyde-3-p	glyceraldehyde-3-p	glyceraldehyde 3-p		qlyceraldehyde-3-p	glyceraldehyde-3-p									

## ALIGNMENTS

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R; Hanauer, A.; Mandel, J.L.
EMBO J. 3, 2627-2633, 1984
A; Title: The glyceraldehyde 3
A; Reference number: A21939; M
A; Accession: A21939
                                                                                                                                A;Residues: 292-310,'V', 312-335 <DAN>
A;Cross-references: GB:M28283; NID:g182978; PIDN:AAA52519.1; PID:g182979
A;Cross-references: GB:M28283; NID:g182978; PIDN:AAA52519.1; PID:g182979
A;Tso, J.Y.; Sun, X.H.; Kao, T.; Reece, K.S.; Wu, R.
Rucleic Acids Res. 13, 2485-2502, 1985
A;Title: Isolation and characterization of rat and human glyceraldehyde-1A;Reference number: A93562; MUID:85215629
A;Accession: B22939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J04038; NID:g182980; PIDN:AAA5 R;Arcari, P.; Martinelli, R.; Salvatore, F. Nucleic Acids Res. 12, 9179-9189, 1984 A;Title: The complete sequence of a full length cDNA A;Reference number: A00365; MUID:85087928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ercolani, L.; Florence, B.; Denaro, M.; Alexander, M. J. Biol. Chem. 263, 15335-15341, 1988
A;Title: Isolation and complete sequence of a functional human A;Reference number: A31988; MUID:89008430
A;Accession: A31988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 08-Dec-1994 #text_change 15-Sep-2000
C;Accession: A31988; A00365; A21939; I53309; B22939; A45924; I55258; A41297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [validated] - human N;Alternate names: triose phosphate dehydrogenase N;Contains: uracil DNA glycosylase (EC 3.2.2.-), nuclear
A;Cross-references: GB:M17851; NID:g182860; PIDN:AAA86283.1; PID:g182861 R;Tokunaga, K.; Nakamura, Y.; Sakata, K.; Fujimori, K.; Ohkubo, M.; Sawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Characterization of the transcription products of glyceraldehyde 3-phosphate A;Reference number: I53309; MUID:85051356
A;Accession: I53309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X01677; GB:K03121; R;Dani, C.; Piechaczyk, M.; Audigier, Y.; Eur. J. Blochem. 145, 299-304, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-224,'D',226-335 <ARC>
A;Cross-references: GB:X01677; GB:K03121; GB:M17851; GB:X01110; NID:g31644; PIDN:CAA2
                                                                   A; Molecule type: mRNA
A; Residues: 2-335 <TSO>
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A; Residues: 1-335 <ERC>
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A; Residues: 1-335 <HAN>
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MUID: 85076585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAA53191.1; PID:g182981
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R; Tokunaga, K.; Nakamura, Y.; Cancer Res. 47, 5616-5619, 19

A; Title: Enhanced expression of a glyceraldehyde-3-phosphate dehydrogenase

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R;Mercer, W.D.; Winn, S.I.; Watson, H.C.

J. Mol. Biol. 104, 277-283, 1976
A;Title: Twinning in crystals of human skeletal muscle D-glyceraldehyde-3-phosphate dehy A;Title: Twinning in crystals of human skeletal muscle D-glyceraldehyde-3-phosphate dehy A;Contents: annotation; X-ray crystallography, 3.5 angstroms
A;Contents: annotation; X-ray crystallography, 3.5 angstroms
Bubmitted to the Brookhaven Protein Data Bank, June 1983
A;Contents: annotation; X-ray crystallography, 3.5 angstroms, residues 2-8, D', 10-40, H. 168-189, S, 191-197, G', 199-202, A', 204-205, L', 207-224, D', 226-242, L', 244-263, E', 265-210, Only one gene appears to be expressed.
             ">"Cross references: GDB:119249; OMIM: A:Map position: 12p13.31-12p13.1 A:Introns: 10/2; 43/3; 79/2; 109/3; 14 C:Complex: homoter crystallizes C:Complex: monomer
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A;Residues: 2-8, 'D',10-40,'H',42-63,'D',65-69,'D',71,'KA',74-82,'EN',85-91,'TA',94-112,'
226-242,'L',244-263,'E',285-278,'DE',281-283,'D',285-287,'GSN',291-293,'I',295-301,'E',
R;Sloud, M; Jespersen, L.
J. Mol. Biol. 257, 775-789, 1996
A;Title: Enhancement of hammerhead ribozyme catalysis by glyceraldehyde-3-phosphate dehy
A;Reference number: S66563; MUID:96194445
A;Accession: S65563
                                                                                                                                                                      A;Gene: GDB:GAPD
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A; Molecule: type: protein
A; Molecule: 2-8, '8',10-23, 'B',25-27;46-47, 'Z',49, 'B',51-61,67-69, 'B',71, 'K'; 'B',82, 'Az',
V',171, 'Zz',174-176, 'SS',179-180, 'AB',186-188, 'B',190-194; 'B',199-202; 'A',204-205, 'L',20
Z',318-321,323-334, 'SKGYK' <NOW>
A; Note: some of this partial sequence was assigned tentatively based on composition
R; Nowak, K.; Wolny, M.; Banas, T.
FBBS Lett. 134, 14-146, 1981
FBBS Lett. 134, 14-146, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 4-15 <SIO>
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A;Residues: 1-193,'NCGYMAA',201,203,'SRTSSLPLL',213,'L',215-329,333-335 <SIR>
A;Residues: EMBL:X53778; NID:g35052; PIDN:CAA37794.1; PID:g35053
R;Nowak, K.; Kuczek, M.; Ostropolska, L.; Malarska, A.; Wolny, M.; Branowski, THOppe-Seyler's Z. physiol. Chem. 356, 1181-1183, 1975
A;Title: The covalent structure of glyceraldehyde-phosphate dehydrogenase from A;Accession: A12103; MUID:76067491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 134, 143-146, 1981
A;Title: The complete amino acid sequence
A;Reference number: A00366; MUID:82073291
A;Accession: A00366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiAllen, R.W.; Trach, K.A.; Hoch, J.A.
J. Biol. Chem. 262, 649-653, 1987
A;Title: Identification of the 37-kDa protein
A;Reference number: I55258; MUID:87109159
A;Accession: I55258
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A; Residues: 1-335 <MEY>
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A; Residues: 1-335 <ALL>
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                    symmetric
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glyceraldehyde-3-phosphate dehydrogenase homolog - rat (fragment) N;Alternate names: glyceraldehyde-3-phosphate dehydrogenase-like | C:Species: Rattus norvegicus (Norway rat) C;Chate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change I:C:Accession: S14477; A24915 R:Krawetz, S.A.; Connor, W.; Dixon, G.H. submitted to the EMBL Data Library, October 1990 A;Accession: S14477 A;Accession: S14477
A;Title: A vector-primer-cloner-sequencer
A;Reference number: A24915; MUID:87053179
A;Accession: A24915
                                                                    A;Cross-references: EMBL:X54798; NID:g57571; PIDN:CAA38569.1; R;Krawetz, S.A.; Connor, W.; Cannon, P.D.; Dixon, G.H.
                                                                  R;Krawetz, S.A.; Connor, W.;
DNA 5, 427-435, 1986
                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-165 < KRAl>
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C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; !
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A:Accession: S26976
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A; Residues: 1-338 <HAR>
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G:Speciles: Agaricus bisporus (cultivated mushroom)
C:Date: 23-Apr.1993 #sequence_revision 23-Apr.1993 #text_cha
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S26976
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A;Description: oxidoreductase; reversibly catalyzes the oxidative phosphorylation A;Pathway: gluconeogenesis; glycolysis
A;Note: tetrameric form; cytosol
C;Function: <NUC>
C;Function: <NUC>
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Pred. No. 0.04
2; Mismatches
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1; Mismatches
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type: mRNA

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Nucleic Acids Res. 18, 3054, 1990
A;Title: Nucleotide sequence of hamster glyceraldehyde-3-phosphate dehydrogenase A;Title: Nucleotide sequence of hamster glyceraldehyde-3-phosphate dehydrogenase A;Reference number: $10221; MUID:90272420
A;Accession: $10221
A;Molecule type: mRNA
A;Residues: 1-333 <VIN>
A;Residues: 1-333 <VIN>
A;Cross-references: EMBL:x52123; NID:g49434; PIDN:CAA36368.1; PID:g49435
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
F;3-33,Region: beta-alpha-beta NAD nucleotide-binding fold
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1
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A; Cross-references:
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Nucleic Acids Res. 1
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11; Conservative
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                                                                              Conservative
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. 18, 3054,
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R; Filipek, A.; Gerke, V.; Weber, K.; Kuznicki, J.

Bur. J. Biochem. 195, 795-800, 1991
A; Title: Characterization of the cell-cycle-regulated protein calcyclin from Ehrlich A; Reference number: S14090; MUID:91153321
A; Accession: S14160
A; Molecule type: protein
A; Residues: 2-20, 'FSCD', 25-26,'D', 28-64,'I', 66-70,'F', 72-77,'F',79-80,'VK',83-86,'D', A; Residues: 2-20, 'FSCD',25-26,'D',28-64,'I', 66-70,'F',72-77,'F',79-80,'VK',83-86,'D', A; Residues: 2-20, 'FSCD',25-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'D',28-26,'
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A; Residues: 1-80, 'AN, '83-304, 'F', 306-333 <TSO>
A; Cross-references: GB: M17701; NID: 9204248; PIDN: AAA41193.1; PID: 920
R; Piechaczyk, M.; Blanchard, J.M.; Marty, L.; Dani, C.; Panableres, Nucleic Acids Res. 12, 6951-6963, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X02231; NID:g56187; PIDN:CAA26150.1; PID:g56188 R;Tso, J.Y.; Sun, X.H.; Kao, T.; Reece, K.S.; Wu, R. Nucleic Acids Res. 13, 2485-2502, 1985 A;Title: Isolation and characterization of rat and human glyceraldehyde A;Reference number: A93562; MUID:85215629 A;Accession: A22939
Biochem. Biophys. Res. Commun. 131, 800-8
A;Title: 1.5 KB mRNA abundantly expressed
A;Reference number: A23280; MUID:86025533
                                                                                                                                                                                                                                                                                       A;Title: Post-transcriptional regulation of glyceraldehyde-3-phosphate-dehydrogenase A;Reference number: A22887; MUID:85014145
A;Accession: A22887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Jun-1999
C;Accession: A23013; A22939; A22887; A23280; A17155; JN0401; A60208; B17155
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                                                                                     R; Maehara, Y.; Fujiyoshi, T.; Takahashi, K.; Biochem. Biophys. Res. Commun. 131, 800-805,
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 261-323 <PIE>
A; Cross-references: GB: X00972
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A; Residues: 1-333 <FOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Fort, P.; Marty, L.; Piechaczyk, M.; El Sabrouty, Nucleic Acids Res. 13, 1431-1442, 1985
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A; Residues: 1-333 <SAB>
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2; Mismatches
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C;Species: Gallus gallus (chicken)
C;Cate: 03-Aug-1984 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: A00368; A32737; A22035; I50231; I50640
R;Dugaiczyk, A.; Haron, J.A.; Stone, E.M.; Dennison, O.E.; Rothblum, K.N.; Schwartz, Biochemistry 22, 1605-1613, 1983
Biochemistry 22, 1605-1613, 1983
A;Cross-references: GB:K01458; NID:g211800; PIDN:AAA48778.1; PID:g211801 R;Stone, E.M.; Rothblum, K.N.; Alevy, M.C.; Kuo, T.M.; Schwartz, R.J. Proc. Natl. Acad. Sci. U.S.A. 82, 1628-1632, 1985 A;Tille: Complete sequence of the chicken glyceraldehyde-3-phosphate dehydrogenase gene A;Reference number: A22035; MUID:85166184
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cloning and sequencing of a deoxyribonucleic A;Reference number: A00368; MUID:83204759
A;Accession: A00368
                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-333 <PAN>
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A; Residues: 235-304, 'F', 306-333 <LEU>
A; Cross references: GB: M29341; NID: g203141; PIDN: AAA40814.1;
A; Experimental source: brain
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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A; Residues: 267-304, 'F', 306-333 < MAE>
A; Cross-references: GB:M11561; NID:9205963; PIDN:AAA41795.1; PID:9205964
R; Vospelnikova, N.D.; Safronova, M.I.; Shuvalova, E.R.; Baratova, L.A.; Kniazev,
Biochem. J. 199, 757-765, 1981
A; Title: Identification of an arginine residue important for catalytic activity
A; Reference number: A90313; MUID:82182080
A; Accession: A17155
A; Cross-reference number: A90313; MUID:82182080
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A;Title: Trifluoperazine activates and releases A;Reference number: A60208; MUID:87224934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Reywords: gluconeogenesis; glycolysis; homotetramer; NAD; F;3-33/Region: beta-alpha-beta NAD nucleotide-binding fold
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A;Title: Peptide sequence containing the active site cysteine of D-glyceraldehyde-3-pho:
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A; Residues: 117-119,'N',121
A; Residues: 8.A.; Zheltova,
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: JN0401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVKVGVNGFGRIGRL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JN0401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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0.056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidoreductase
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A;Gene: gapdh
C;Complex: homotetra
C;Complex: monomer
C;Function: <CYT>
                     A; Pathway: gluconeogenesis; glycolysis
A; Note: tetrameric form; cytosol
C; Function: <NUC:
A; Description: DNA repair; uracil DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: I46471; MUID:83167564
A;Accession: I46482
A;Starno.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-333 <APP>
A; Cross-references: GB:L23961; NID:g406106; PIDN:AAA85218.1;
A; Experimental source: spleen
R; Putney, S.D.; Herlihy, W.C.; Schimmel, p.
Nature 302, 718-721, 1983
A; Title: A new troponin T and cDNA clones for 13 different mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - ra
N;Alternate names: triose phosphate dehydrogenase
N;Contains: uracil DNA glycosylase (EC 3.2.2.), nuclear
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_ch
C;Accession: JC4309; I46482
R;Applequist, S.E.; Keyna, U.; Calvin, M.R.; Beck-Engeser,
Gene 163, 325-326, 1995
A;Title: Sequence of the rabbit glyceraldehyde-3-phosphate
A;Accession: JC4309; MUID:96011658
A;Accession: JC4309; MUID:96011658
                                                                                                                                                                              A; Description: oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 33-79 < PUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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A; Introns: 8/2; 41/3;
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A;Residues: 'G',198-276,'E',278-328,'T',330-333 <AR2>
A;Cross-references: EMBL:V00406; NID:g63400; PIDN:CAA23697.1; PID:g63401
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A;Rosidues: 1-293,'H',295-333 <STO>
A;Rosidues: 1-293,'H',295-333 <STO>
A;Cross-references: GB:M11213; NID:g211796; PIDN:AAA48774.1;.PID:g211797
A;Note: the authors translated the codon CAT for residue 294 as Asp
R;Arnold, H.H.; Domdey, H.; Wiebauer, K.; Datta, K.; Siddiqui, M.A.Q.
J. Biol. Chem. 257, 9872-9877, 1982
A;Title: Cloning, partial sequencing, and expression of glyceraldehyde-3-phosphate A;Accession: I50231; MUID:82265644
A;Accession: I50231
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4;Residues: 'G',198-276,'E',278-333 <ARN>
A;Cross-references: GB:J00848; NID:9211798; PIDN:AAA48777.1;
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12; Conserv
DNA repair; uracil DNA glycosylase
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle proteins,
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monomeric

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A; Experimental source: skeletal muscle
R; Soukri, A.; Hafid, N.; Valverde, F.; Elkebb
Biochim. Biophys. Acta 1292, 177-187, 1996
A; Title: Evidence for a posttranslational cov
A; Reference number: S62673; MUID: 96139342
A; Accession: S62674
A; Molecule type: protein
A; Residues: 2-26 <SOU>
C; Genetics:
                                                                                                                                                                                       JN0678

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) -
C:Species: Coturnix coturnix (quail)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text.
C:Accession: JN0678; S35726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: gapC
C;Complex: homotetramer
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; hibernation; homotetramer;
C;Keywords: glyceraldehyde-3-phosphate dehydrogenase #status ex
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                                  A; Molecule type: mRNA
A; Regidues: 1-333 <WEI>
A; Cross-references: GB: Z19086;
C; Genetics:
                                                                                                      Gene 128, 269-272, 1993
A;TItle: Sequence and expression of a glyceraldehyde-3-phosphate
A;Reference number: JN0678; MUID:93292997
A;Accession: JN0678
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                                                                                                                                                            R; Weiskirchen, R.; Siemeister, Gene 128, 269-272, 1993
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A; Residues: 1-333 <SOU1>
A; Cross-references: EMBL: X87226;
A; Accession: PC4314
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Gene 181, 139-145, 1996
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Best Local S
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12; Conserv
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12; Conser
glyceraldehyde-3-phosphate dehydrogenase
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                                                                                                                                                                              G.; Hartl,
                                                     NID: g62615;
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Pred. No. 0.05
2; Mismatches
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0.056;
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A;Introns: 4/3; 21/2; 42/3; 271/1
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase C;Keywords: gluconeogenesis; glycolysis; homotetramer; P;4-34/Region: beta-alpha-beta NAD nucleotide-binding fc F;151,178/Active site: Cys, His #status predicted
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C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase

C;Keywords: gluconeogenesis; glycolysis; homotetramer; r

F;4-34/Region: beta-alpha-beta NAD nucleotide-binding fr

F;151,178/Active site: Cys, His #status predicted
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Nucleic Acids Res. 18, 5566, 1990
A:Title: Nucleotide sequence of the glyceraldehyde-3-phosphate A:Title: Nucleotide sequence of the glyceraldehyde-3-phosphate
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                                                                                                                                                                                                                                                                                                                           A; Title: Genome analysis of imperfect fungi: A; Reference number: S17981; MUID:92035062 A; Accession: S17981
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Curr. Genet. 20, 151-155, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) -
C;Species: Curvularia lunata
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_
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A; Introns: 42
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A; Residues: 1-337 <OSI>
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A; Residues: 1-337 <CHO>
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C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase
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R/Sahni, M.; Kinsey, J.A.
submitted to the EMBL Data Library, April 1996
A/Description: Isolation of the Neurospora crassa glyceraldehyde-3-phosphate dehydrogena
                                                                                                                                                                                                                      C;Genetics:
A;Gene: gpd-1
                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/D
A;Molecule type: mRNA
A;Residues: 1-338 <SAH>
A;Cross-references: EMBL:U56397; PIDN:AAB00570.1
                                                                                                                                                                                                                                                                                                                            A; Reference number: Z24398
A; Accession: T47218
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A;Introns: 4/3; 21/2; 42/3; 271/1
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1991
A;Reference number: $22150
A;Accession: $22150
A;Molecule type: DNA
A;Residues: 1-21,'HRADRRRHCRRKR',35-36,'HRAPLRS',44-337 <YOD>
A;Cross-references: EMBL:X63516
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A;Residues: 1-337 <VAND
A;Residues: 1-337 <VAND
A;Cross-references: EMBL:X63516; NID:g2581; PIDN:CAA45084.1; PID:g2582
A;Note: the authors translated the codon GAC for residue 28 as Arg, AAG for residue 56
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A;Reference number: S26946; MUID:92306164
A;Accession: S26946
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                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Neurospora crassa
;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
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G3P_TRIHA	G3P_COLGL	G3P_LACLA	G3P_COLLN	G3P2_TRIKO	G3P1_AGABI	G3P_STRPY	G3P_STREQ	G3P_RAT	G3P_RABIT	G3P_PIG
P87197	P35143									P00355
trichoderma	colletotric	lactococcus	colletotric	trichoderma	agaricus bi	streptococc	streptococc	rattus norv	oryctolagus	sus scrofa

## ALIGNMENTS

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G3P2_HUMAN
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-85076585; PubMed-6096136;

Hanauer A., Mandel J.L.;

"The glyceraldehyde 3 phosphate d
of a human cDNA and of an X chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-89008430; PubMed-3170585;

Ercolani L., Florence B., Denaro M., Alexander M.

"Isolation and complete sequence of a functional glyceraldehyde-3-phosphate dehydrogenase gene.";

Biol. Chem. 263:15335-15341(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (EC 1.2.1.12).
                                 "A human nuclear uracil DNA glycosylase is the 37-kDa glyceraldehyde-3-phosphate dehydrogenase."; proc. Natl. Acad. Sci. U.S.A. 88:8460-8464(1991).
                                                                                                                                                                                               Arcari P., Martinelli R., Salvatore F.;
"The complete sequence of a full length cDNA for human liver glyccraldehyde-3-phosphate dehydrogenase: evidence for multip
                                                                                                                                                                                                                                                                                        "The glyceraldehyde 3 phosphate dehydrogenase of a human cDNA and of an x chromosome linked complexity of the gene family in mouse."; EMBO J. 3:2627-2633(1984).
                                                                                                                                                                                                                                                                                                                                                                                                         phosphate dehydrogenase cDNAs: genomic evolution of the gene.";
Nucleic Acids Res. 13:2485-2502(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
MEDLINE-85215629; PubMed-2987855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A.
                                                                                 Sirover M.A.;
                                                                                                         MEDLINE=92020872;
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                                                                                             Meyer-Siegler K., Mauro
                                                                                                                             TISSUE=Placenta;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                      species.";
                                                                                                                                                                                                                                              MEDLINE=85087928; PubMed=6096821;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tso J.Y., Sun X.-H.,
                                                                                                                                                                      Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                      Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                           PubMed=1924305;
Mauro D.J., Seal
                                                                                                                                                                      12:9179-9189(1984).
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and human glyceraldehyde-3-
complexity and molecular
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                                                                                           J.,
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pseudogene;
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                                                                                              Deriel J.K.,
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EMBL; M17851; AAA86283.1; ...
EMBL; X01677; CAA25833 1; ...
EMBL; J04038; AAA53191.1; ...
EMBL; X53778; CAA37794 1; ...
EMBL; M33197; AAA52518.1; ...
EMBL; M33197; AAA52518.1; ...
EMBL; AF261085; AAA59678.1; ...
EMBL; AF261085; AAF99678.1; ...
EMBL; AY007133; AAG01996.1; ...
EMBL; AY007133; AAG01996.1; ...
EMBL; AY007133; AAG01996.1; ...
EMBL; AY007133; AAG01996.1; ...
                       HSSP; P00354; 3GPD.
SWISS-2DPAGE; P04406; HUMAN.
Aarhus/Ghent-2DPAGE; 1206; NEPHGE.
HSC-2DPAGE; P04406; HUMAN.
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                                                                                    PIR; A41297; A41297.
PIR; A45924; A45924.
                                                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                             use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electrophoresis 16:1160-1169(1995).

- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH.

- NAD(+) - 1, 3-DIPHOSPHATEGLYCERATE + NADH.

- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

- SUBCUNITY HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The major protein expression profile and two-dimensional protein database of human heart,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96007936; PubMed-7498159;
Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova
Ershova E.S., Egorov T.A., Musalyamov A.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Zhou J., Yu W., Tang Margolin J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cDNA cloning by amplification of circularized first reveals non-IRE-regulated iron-responsive mRNAs."; Biochem. Biophys. Res. Commun. 275:223-227(2000).
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MEDIJINE-87109159; PubMed-3027061;
Allen R.W., Trach K.A., Hoch J.A.;

"Identification of the 37-kDa protein displaying interaction with the erythroid cell membrane as glyceraldehyde-3-phosphate dehydrogenase.";

Biol. Chem. 262:649-653(1987).
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Ye Z., Connor J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Res. 47:5616-5619(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tokunaga K., Nakamura
Sawada K., Sakiyama S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88026722;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                            European
                                                                                                                  B22939; B22939.
A21939; A21939.
A31988; A31988.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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an email to license@isb-sib.ch).
IPR000173;
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mura Y., Sakata
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G3P2_AGABI
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Best Local S
Matches 13
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INIT_MET 0 0
BINDING 151 151 G
ACT_SITE 178 178 A
CONFLICT 224 224 N
SEQUENCE 334 AA; 35922 MW:
         ACT_SITE SEQUENCE
                                   Glycolysis;
BINDING
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                          EMBL; M81728; AAA32634.1;
PIR; S26976; S26976.
                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       + NAD(+) = 1,3-DIPHOSPHATEGIYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE

-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-!- SUBUNIT: HOMOTETRAMER.
                                                               PROSITE;
                                                                            PRINTS;
                                                                                      Pfam; PF00044; gpdh; 1.
                                                                                                   HSSP; P00357; 1GPD.
InterPro; IPR000173;
                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE GLYCERA
DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAINE-93113715; PubMed-1473176; MEDLINE-93113715; PubMed-1473176; MC., Schuren F.H.J., Mou
                                                                                                                                                                                                                                                                                                                                                                     chrysosporium and Agaricus bisporus.";
Curr. Genet. 22:447-454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agaricus bisporus (Common mushroom).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
Agaricaceae; Agaricus.
NCBI_TaxID=5341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT 1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC
                                                                                                                                                                                                                                                                                                                                                                                                  genes from the basidiomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                              Harmsen M.C.,
Wessels J.G.H.
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P32636;
                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
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                                                           PR00078; G3PDHDRGNASE; PS00071; GAPDH; 1.
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13; Conservative
Oxidoreductase; NAD; Multigene family.
150 150 GLYCERALDEHYDE 3-PHOSPHATE.
177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
338 AA; 36570 MW; 3381DBBF73B84469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Pred. No.
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0.025;
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P33898;
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92011371; PubMed-1917845;
Hidalgo E., Chen Y.-M., Lin E.C.C., Aguilar
"Molecular cloning and DNA sequencing of th
ald gene encoding aldehyde dehydrogenase.";
J. Bacteriol. 173:6118-6123(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Creat
01-FEB-1994 (Rel. 28, Last
15-JUL-1999 (Rel. 38, Last
GLYCERALDEHYDE 3-PHOSPHATE
EcoGene; EG12103; gapC.
InterPro; IPR000173; -.
Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                   EMBL; L09067; AAA23856.1; ALT_FRAME.
EMBL; M64541; -; NOT_ANNOTATED_CDS.
EMBL; X07569; -; NOT_ANNOTATED_CDS.
HSSP; P17721; 1HDG.
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                                                                                                                                                                          DEHYDROGENASE FAMILY.

DEHYDROGENASE FAMILY.

CAUTION: THIS IS A CONCEPTUAL TRANSLATION; FRAMESHIFTS

BE INTRODUCED TO PRODUCE THIS ORF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Limon A., (XXX-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria;
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annotation update)
DEHYDROGENASE C (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision;
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                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aguilar J.;
                                                                                                                                                                                                                                                                                                                                                                  Anraku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332
                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                        encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                        cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2.1.12) (GAPDH-C).
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                                                                                                                                                 restrictions
                                                                                                                                                            EMBL
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                                                                                                                                                             a collaboration -
                                                                                                                                                                                                      HAD
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                                                                                                                                                            outstation
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RESULT 4
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Query Match
Best Local S
Matches 12
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
01-APR-1993
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                               van Wert S.L., Yoder O.C.;
"Structure of the Cochliobolus heterostrophus
"Structure of the cochliobolus heterostrophus gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G3P
                                                       Glycolysis; Oxidoreductase; NAD.
BINDING 151 151
BINDING 151 151
ACTIVATES THIOL GROUP DURING SEQUENCE 337 AA; 36544 MW; ABAF2743A362743E CRC64;
                                                                                                                                                    EMBL; X63516; CAA45084.1;
PIR; S22150; S22150.
PIR; S26946; S26946.
HSSP; P00357; IGPD.
                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cochliobolus heterostrophus (Drechslera maydis). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dc Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycolysis; Oxidoreductase; NAD; Multigene : BINDING 150 150 GLYCERALDEHYDE
                                                                                                       InterPro; IPRO00173; -.
pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 48330 / C3;
MEDLINE=92306164; PubMed=1339326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC SIMILARITY: BELONGS TO THE GLYCER DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCHE
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 l Similarity
12; Conser
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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            61.5%;
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72.2%;
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                                                                                                                                                                                                                                                                                                                          THE GLYCERALDEHYDE 3-PHOSPHATE
 ?:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB Pred. No. 0.04
3; Mismatches
            Score
Pred.
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ACTIVATES THIOL GROUP DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3Y SIMILARITY).
C99B5389697E001E CRC64;
 Mismatches
           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
             0
            DB 1;
0.048;
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0.047;
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E 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2.1.12) (GAPDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dothideomycetes;
                       Length 337;
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  Indels
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                                                                                                                                                                                                                                                              restrictions
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                                                                      CATALYSIS
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RESULT
G3P_CRYPA
ID G3P_CRYPA
P19089;
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Best Local S
Matches 12
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InterPro; IPR000173; -
Pfam; PF00044; 9pdh; 1.
PRINTS; PR00078; G3PDHDH; 1.
G1yColysis; Oxidoreductase; NAb.
BINDING 178 178 ACTIVE
SEQUENCE 337 AA; 36194 MW; 38C
                                                     G3P_CURLU
P28844;
P1-DEC-1992
01-DEC-1992
01-DEC-1999
                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC
    Eukaryota;
                   Curvularia
                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X53996; CAA37943.1; PIR; S11447; DEJJGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene from Cryphonectria parašitica.";
Nucleic Acids Res. 18:5565-5565(1990).
-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
-I- PATHAAX: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GPD-1).
Cryphonectria parasitica (Chesnut blight fungus) (Endothia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-91016863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasitica).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diaporthales;
                                                                                                                                                                              N
                                                                                                                                                                                                   3 LYLYGVNGFGRIGRI 17
                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTETRAMER.
SUBCELULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                           VVKVGINGFGRIGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                l Similarity
12; Conserv
    Fungi; Ascomycota;
                 lunata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuss D.L.;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              DEJJGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valsaceae;
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-2216743;
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                                                                                                                                                                                                                                        61.5%;
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                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                         Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                        GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING
; 38C8C04A557E68E6 CRC64;
 Pezizomycotina;
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                             Mismatches
                                                                                                         337
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0.048;
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                                      1.2.1.12) (GAPDH).
Dothideomycetes
                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                   Length 337;
                                                                                                                                                                                                                            Indels ·
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                                                                                                                                                                                                                                                                                                      CATALYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outstation
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RESULT 7
G3P_LYOSH
ID G3P_LY
AC 09224
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                                                                                                                                                                                                                                                                                                                                                                                     G3P_LYOSH
G3P_LYOSH
G92243;
092243;
01-NOV-1997 (Rel. 35, Created)
r 01-NOV-1999 (Rel. 35, Last seque
T 15-JUL-1999 (Rel. 38, Last anno
T 15-JUL-1999 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 12
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PIR; S17981; DEXDGC.
HSSP; P00357; IGPD.
InterPro; IPR000173; -.
Pfam; PF00044; gpdh; 1.
PROSITE; PR00078; GAPDH; 1.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                        Lyophyllum shimeji.
Eukaryota; Fungi; Ba
Tricholomataceae; Ly
NCBI_TaxID=47721;
          SEQUENCE FROM N.A.

SALTO T., Tanaka N., Toyomasu T.;

Submitted (NOY-1996) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + C

+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSI

-!- SUBUNIT: HOMOTETRAMER (BY STMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SUMLIARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF
-!- SUBUNIT: HOMOTEPRAMER.
-!- SUBCELLULAR LOGARTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osiewacz H.D., Ridder R., "Genome analysis of imperfect further characterization of the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LVLVGVNGFGRIGRI 17
  DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
178
337 }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA;
                                                                                                                                                                                                                                                                                                                            Basidiomycota; Hymenomycetes; Agaricales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
: 36549 MW;
                                                                                                                                                                                                                                                                                                              Lyophyllum.
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                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
DEHYDROGENASE (EC
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCERALDEHYDE 3-PHOSPHATE ACTIVATES THIOL GROUP DURIL; BF79C6D673647A07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                     GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
No.
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0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                           1.2.1.12) (GAPDH).
                                                                                            GLYCOLYSIS
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                                                                                                                                                   ORTHOPHOSPHATE
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Dunlap J.C., Shinohara M.L., Bell-Pedersen D., Loros J.J

Bunlap J.C., Shinohara M.L., Bell-Pedersen D., Loros J.J

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + (

+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

PTDCM STECM STEP IN THE SECOND PHASE OF GLYCOLYS.
                                                                                             entities or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G3P_NEUCR STANDARD; PRT; 338 AA. P54118; Q92255; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38-PHOSPHATE DEHYDROGENASE (ECC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructed the companies of the companies of the contract of the companies o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sahni M., Kinsey J.A.; "Identification and clor phosphate dehydrogenase
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BINDING 150 150 GLY
ACT_SITE 177 177 ACT
SEQUENCE 337 AA; 36724 MW; D
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NCBI_TaxID=5141;
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Eukaryota, Fungi, Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
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PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
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Local Similarity 80.0%;
hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                      PATHWAY: FIRST STEP IN THE SECOND PHASE SUBUNIT: HOMOTETRAMER (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE GLYCERALDEHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                               DEHYDROGENASE FAMILY.
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                       U56397;
U67457;
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                                                                                             non-profit institutions as long and this statement is not removed requires a license agreement (see an email to license@isb-sib.ch).
AAB00570.1;
AAB95425.1;
1GPD.
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                                                                                                                                                                                                                                                                                                                         BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning of the Neurospora nase gene, gpd-1.";
44:47-49(1997).
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Pred. No. 0.04
2; Mismatches
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0.048;
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MBL outstation -
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Pl_JACOR
STANDAKU;
G3Pl_JACOR
STANDAKU;
C P80534; Q64418;
C P80534; Q64418;
T 01-FEB-1996 (Rel. 33, C:
DT 01-NOV-1997 (Rel. 35, I:
T 1-TIT,-1999 (Rel. 38, I:
T 1-PHOSP
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Best Local S
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CONFLICT
SEQUENCE
                                                                                  entities
or send a
                                                                                                                                             This SWI
between
                                                                                                                                                                                                                                                      Induced hibernating jerboa (Jaculus orientalis).";
Gene 181:139-145(1996).
-i- CATALYTIC ACTIVETY.
            Pfam; PF00044; gpdh; PRINTS; PR00078; G3P
                                              EMBL; X87226; CAA60678.1; HSSP; P00354; 3GPD.
                                                                                                          modified
                                                                                                                        use
                                                                                                                                  the
                                                                                                                                                                                                                                                                                          MEDLINE-97128782; PubMed-0973322;
SOUKri A., Valverde F., Haifd N., Elkebbaj M.S., Serrano A.;
"Occurrance of a differential expression of the glyceraldehyde-3-
phosphate dehydrogenase gene in muscle and liver from euthermic ar
                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skeletal muscle;
Soukri A., Serrano A.;
Submitted (JAN-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycolysis;
BINDING
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Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                  InterPro; IPR000173; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GAPDH).
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CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
SUBBUIT: HOMOTETRAMER.
SUBBUIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.

SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restropy by non-profit institutions as long as its content
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12; Conserv
                                                                                 non-profit institutions as long as its content is d and this statement is not removed. Usage by and for removed as requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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338
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212
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Rel. 38, Last
Rel. 38, Last
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212
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Rodentia;
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annotation update)
DEHYDROGENASE, MUSCLE
                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT
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GLYCERALDEHYDE 3-PHOSPHATE
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Pred.
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DA -> ER (IN REF. 2)
A -> S (IN REF. 2)
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ACTIVATES THIOL GROUP DURING
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No. 0.048;
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RESULT 10
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Best Local S
Matches 12
                       EMBL; X07156; CAA30151.1;
EMBL; X15596; CAA33620.1;
PIR; S00354; DEZMGC.
PIR; S06879; S06879
HSSP; P00357; 1GPD.
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                                                                                                                                                                                                                               modified
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1: CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH. + NADH. + 1.3-DIPHOSPHATECLYCERATE + NADH. - 1.5-DIPHOSPHATESTYCERATE + NADH. - 1.5-DIPHOSPHATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCERATESTYCHATESTYCERATESTYCERATEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90040690; PubMed=2810356;
Martinez P., Martin W.F., Cerff R.;
"Structure, evolution and anaerobic regulation of a nuclear
encoding cytosolic glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                         or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chloroplast glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88230473; PubMed=3131533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. W22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideac
Andropogoneae; Zea.
     MaizeDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: ELD. ...
SUBGNIT: HOMOTETRAMER.
SUBGRILDLAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
MISCELLANEOUS: PLANTS CONTAIN THREE FORMS OF GAPDH: A CYTOSOLIC MISCELLANEOUS: PLANTS CONTAIN THREE FORMS TORMS WHICH PARTICIPATES IN GLYCOLYSIS AND TWO CHLOROPLAST FORMS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
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                                                                                                                                                                                                                                                                                                                                                                                                    FORM WHICH PARTICIPATES IN GLYCOLYSIS WHICH PARTICIPATES IN PHOTOSYNTHESIS. ENCODED BY DISTINCT GENES.
SIMILARITY: BELONGS TO THE GLYCERALDEH
                                                                                                                                                                                                                                                                                                                                                                               DEHYDROGENASE FAMILY
                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVKVGVNGFGRIGRL 15
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                                                                                                                                                                         non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 AA;
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    TO THE GLYCERALDEHYDE 3-PHOSPHATE
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Pred.
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ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
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0.051;
                                                                                                                                                                                                http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                     Usage
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RESULT 11
G3PC_MESCR
ID G3PC_MESCR
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Best Local Similarity 62.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P17878;
P17878;
P17878;
O1-AUG-1990 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
CTYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE CONFLICT SEQUENCE
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                       EMBL; J05223; AAA33033.1;
EMBL; M29956; AAA33031.1;
PIR; A35080; A35080.
HSSP; P00357; 1GPD.
                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 265:3497-3502(1990).

-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.

-I- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                             Ostrem J.A., Vernon D.M., Bohnert H.J.;
"Increased expression of a gene coding for NAD:glyceraldehyde-3-
phosphate dehydrogenase during the transition from C3 photosynthesis
to crassulacean acid metabolism in Mesembryanthemum crystallinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Trache Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesembryanthemum crystallinum (Common ice plant). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: FIRST STEP IN
-!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=90154012; PubMed=2303458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00078; G3PDHDRGNASE. PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00044; gpdh; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3544;
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                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC.
MISCELLANEOUS: PLANTS CONTAIN THREE FORMS OF GAPDH: A CYTOSOLIC FORM WHICH PARTICIPATES IN GLYCOLYSIS AND TWO CHLOROPLAST FORMS WHICH PARTICIPATES IN PHOTOSYNTHESIS. THESE THREE FORMS ARE
                                                                                                                                                                                                                                            ENCODED BY DISTINCT GENES.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
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154
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R000173: -
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Pred. No. 0.06
4; Mismatches
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GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING
T -> S (IN REF. 2).
; E18F580F09FDC07B CRC64;
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Caryophyllidae;
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Mendel; 74; MEScr;GapC;1.
InterPro; IPR000173; -.

PF00044; gpdh; s; PR00078; G3P

G3PDHDRGNASE

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RESULT 12
G3PC_ORYSA
ID G_3PC_O
AC Q4297/
DT 15-JUL
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Best Local S
Matches 13
   Query Match
Best Local S
Matches 10
                                 endel; y.a.,
interPro; IPRO0017,
interPro; IPRO0017,
interPro; IPRO0017,
interPro; IPRO0017,
interPro; IPRO0017,
interPro; IPRO004; 1
interPro; IPRO007,
interPro; IPRO0017,
interPro; IPRO
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DOMAIN
BINDING
ACT_SITE
SEQUENCE
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Q42977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                EMBL; U31676; AAA82047.1; -
HSSP; P00357; 1GPD.
Mendel; 9724; ORYsa;GapC;1.
InterPro; IPR000173; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS
Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAPC OR GPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTETRAMER.
SUBCELLAULAR LOCATION: CYTOPLASMIC.
SUBCELLAUGUS: PLANTS CONTAIN THREE FORMS OF GAPDH
MISCELLANGUS: PLANTS IN GLYCOLYSIS AND TWO CHLC
FORM WHICH PARTICIPATES IN PHOTOSYNTHESIS. THESE THREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENCODED BY DISTINCT GENES. SIMILARITY: BELONGS TO THE GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEHYDROGENASE FAMILY
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13; Conser
                              Similarity
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1 151

152 337

154 154

181 181

181 181

337 AA; 36587 MW
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         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Rel. 36, Last s
Rel. 38, Last s
3-PHOSPHATE I
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                              60.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation update)
DEHYDROGENASE, CYTOSOLIC
   Score 63; DB
Pred. No. 0.06
4; Mismatches
      4
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BINDING TO NAC
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Pred.
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CATALYTIC.

GLYCERALDEHYDE 3-PHOSPHATE.

ACTIVATES THIOL GROUP DURING CATALYSIS.

B07B2BA25509E9EA CRC64;
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(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
0.066;
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0.066;
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   Indels
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Mendel: 575; ZEAma;GapC;2.
InterPro; IPR000173; -.
Pfam; PF00044; gpdh; 1.

PR00044; gpdh; 1. PR00078; G3PDHDRGNASE.

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RESULT 13
G3PD_MAIZE
EMBL; U45858; AAA87880.1; --
EMBL; X73151; CAA51676.1; --
EMBL; U45855; AAA87578.1; --
EMBL; L13432; AAA33466.1; --
Mendel; 575; ZEAma;GapC; 2.
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
-!- PATHMAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: DEVELOPING SEED, SEEDLING ROOTS AND SHOOTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 91-337 FROM N.A.
STRAIN-CV. BERKELEY FAST; TISSUE-Coleoptile;
MEDLINE-92393412; PubMed-2535522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization and promoter analysis of
cytosolic glyceraldehyde 3-phosphate dehydrogenase
expression during anoxia.";
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Magnoliophyta; Liliopsida;
Andropogoneae; Zea.
                                                                                                                                           entities requires a license agreement (See http://www.isb-sib
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glyceraldehyde-3-phosphate dehydrogenase
Plant Cell 1:793-803(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Differential expression and sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1996) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: PLANTS CONTAIN THREE FORMS OF GAPDH: A CYTOSOLIC FORM WHICH PARTICIPATES IN GLYCOLYSIS AND TWO CHLOROPLAST FORMS WHICH PARTICIPATES IN PHOTOSYNTHESIS. THESE THREE FORMS ARE
                                                                                                                                                                                                                                                                                                                                                 ENCODED BY DISTINCT GENES.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                     DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND EMBYRO MATURATION.
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
YDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
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; Poales; Poaceae; PACC clade; Panicoideae
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family.";
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Matches 10
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Best Local
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                                                                                                                                                                          EMBL; X60343; CAA42901.1; -.
PIR; S18482; DEBHG.
HSSE; PO0357; IGPD.
HSSE; PO0357; IGPD.
Mendel; 8661; HORVU;GapC;4.
InterPro; IPR000173; -.
Pfam; PF00044; gpdh; 1.
Pfam; PF00071; G3PDHDRGNASE.
PRINTS; PR00078; G3PDH; 1.
G1yCO1ys1s; Oxidoreductase; NAD; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO
Glycolysis;
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P26517;
01-AUG-1992
01-AUG-1992
15-JUL-1999
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin W., Gierl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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GLVLVGVNGFGRIGRI 17
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| GKIKIGINGFGRIGRL 17
                                                    . Similarity
10; Conserv
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α,
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62.5%;
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Poales; Poaceae; Pooideae; Triticeae;
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                                                 Score 63; DB 1;
Pred. No. 0.066;
4; Mismatches
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BINDING TO NAD.

CATALYTIC.

GLYCERALDEHYDE 3-PHOSPHATE.

ACTIVATES THIOL GROUP DURING CATALYSIS.

05E78CD87964F244 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; D
Pred. No. 0.
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0.066;
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                                                                                                   Length 337
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                                                 Indels
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Search completed: June 13, 2001, Job time: 528 sec
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Q00584;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUIT. Genet. 25:101-106(1994).

-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH.

-!- NAD(+) = 1,3-DLPHOSPHATEGLYCERATE + NADH.

-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-!- SUBUNIT: HOMOTEGRAMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X73282; CAA51721.1;
HSSP; P00357; 1GPD.
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NCBI_TaxID=5111;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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                                                                                                                                                                                     4 VLVGVNGFGRIGRI
                                                                                                                                                                                                                                                                                               Match
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178
337 1
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36029 MW;
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85.7%;
                         14:30:38
                                                                                                                                                                                                                                                                Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING; 1C2360B9701E26B9 CRC64;
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0.066;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374700
o97653 equus cabal
o97652 felis silve
Q9mz05 ovis aries
Q41949 arabidopsis
Q9m8w8 arabidopsis
o04231 selaginella
Q9y7h1 piromyces s
Q9uvc0 pichia cife
                                                                        O9uw96 pleurotus s
O9p80 phaeosphaer
O9y8e9 cryptococcu
O9ptw5 paralichthy
O9uv42 phaffia rho
O9uv42 phaffia rho
O9uv52 streptococc
                                                                                                                                               Q03850 rattus norv
Q9n2d6 canis famil
Q9n2d5 felis silve
                                                                                                                                                                                   Description
                                                                                                                                      Q9qwu4 rattus norv
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
58.5	59	59	59	59	59	59	59	59	59	59	59.	59	59	59	60	60	60	60	60	60	60	61	61	61	61
56.2	56.7	56.7	•	•	•	•	56.7	•	•		•	56.7	56.7	56.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	58.7	58.7	58.7	58.7
388	615	614	363	363	361	353	339	338	338	337	3 3 3	330	320	32	361	338	337	333	83	49	17	422	368	339	337
10	10	10	S	Ç	տ							N	N	u	G	N	10	N	Ľ	თ	σ	10	10	10	ω
004167	Q9M7R5	Q9LE93	Q26754	Q26753	096423	Q43311	Q9N655	Q27,776	001373	Q43359	Q9WWL7	Q9RUP1	Q9L5X6	Q9NJT5	096424	032755	Q9xG67	Q9KT36	P97617	P90514	Q9TQZ5	Q9SAJ6	065843	Q9M7R9	Q9Y796
004167 pyrenomonas	Q9m7r5 odontella s	Q91e93 phaeodactyl	Q26754 trypanoplas	Q26753 trypanoplas	096423 crithidia f	Q43311 euglena gra		Q27776 schistosoma	001373 schistosoma	Q43359 zea mays (m	Q9wwl7 synechococc	Q9rupl deinococcus	Q915x6 streptococc	Q9njt5 leishmania	096424 herpetomona	032755 lactobacill	Q9xg67 nicotiana t	Q9kt36 vibrio chol	P97617 rattus norv		3	Q9saj6 arabidopsis	065843 marsilea qu	Q9m7r9 achlya bise	Q9y796 cryptococcu

## ALIGNMENTS

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RESULT
Q03850
NAD; NADP
NON_TER
SEQUENCE
                                                                                                                                                                                                  MEDLINE-87053179; PubMed-3780374; Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.; "A vector-primer-cloner-sequencer plasmid for the construction libraries: evidence for a rat glyceraldehyde-3-phosphate dehydrogenase-like mRNA and a ferritin mRNA within testis."; DNA 5:427-435(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-NOV-1996 (TrembLrel. 13, Last annotation update)
01-MAY-2000 (TrembLrel. 13, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+) (EC 1.2.1.13)
(TRIOSEPHOSPHATE DEHYDROGENASE (NADP+)) (RAT GLYCERALDEHYDE-3-
                                          + NAD(+) - 3 -PHOSPHO-D-GLYCEROYL PHOSPHATE + NADPH.

EMBL; X54798; CAA38569.1; -.

EMBL; M14165; AAA41178.1; -.

HSSP; P17721; 1HDG;

INTERPRO; IPRO00173; -.

INTERPRO; IPRO00531; -.

PFAM; PF00044; gpdh; 1.

PROSITE; PS00071; GAPDH; 1.

PROSITE; PS000430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-SPRAGUE DAWLEY; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-52 FROM N.A.
                                                                                                                                                                                                                                                                                                                             Krawetz S.;
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G3PD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q03850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHATE DEHYDROGENASE) (FRAGMENT).
                                                                                                                                                                                    CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
                                NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Q63208;
                                                                                                                                                                                                                                                                                                                            (OCT-1990) to the EMBL/GenBank/DDBJ databases
 165 AA;
                165
 165
17737
 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
 EAE35E4B8E705A02 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
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Q9N2D5
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Best Local S
Matches 12
                                                       Query Match
Best Local :
                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUS-ADRENAL GLAND;
Kitamura H., Adachi K., Kido N., Hagiya T., Minase K., Yasui H.,
Yano E., Ohta Y., Tabu K., Mae J., Kanehira K., Ohashi A.;
"Canine glyceraldehyde-3-phosphate dehydrogenase (GAPDH), comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                    Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AB038241; BAA90818.1; -. SEQUENCE 333 AA; 35813 MW; 20501C401BBE790
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-WHITE ADITOSE TISSUE;
Kitamura H., Adachi K., Ohta Y., Kido N., Hagiya
Yano E., Minase K., Mae J., Tabu K., Kanehira K.,
"Feline glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB038240; BAA90817.1; - SEQUENCE 333 AA; 35861 MW; E08B4C39FA2AF7EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9N2D5;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9685;
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13; Conser
                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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72.2%;
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                                                       61.5%;
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Pred.
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Pred. No. 0.19;
2; Mismatches
                                                       Score 64; DB 6
Pred. No. 0.19;
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; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                       20501C401BBE7906 CRC64;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                              N., Hagiya T., Yasui H.,
Kanehira K., Ohashi A.;
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0.086;
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                                                                                        Length 333;
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AC Q9UW96;
AC Q9UW96;
AC Q9UW96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-CCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLYCEROL-3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
OS Pleurotus sajor-caju (Oyster mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
D1-aurotaceae; Pleurotus.
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Q9QWU4
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Q9QWU4;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                               Jeong M.-J., Park S.-C., Byun M.-O., Ryu J.-C.;
"Isolation and characterization of the gene encoding glycerol-3-
phosphate dehydrogenase from Pleurotus sajor-caju.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APO87676; AAD52091.1;
HSSP; P56649; 1DSS.
HXTERPRO; IPRO000173;
-PFAM; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
NON_TER 335 335
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HSSE; P00354; 3GPD. HSSE; P00354; 3GPD. INTERPRO; IPR000173; -
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PRINTS; PR00078; G3PDHDRGNASE.
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Mammalia; Eutheria;
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STRAIN-ASI2070; TISSUE-MYCELIA;
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DEHYDROGENASE (EC 1.2.
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Best Loc
Matches
Best Local Similarity Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                          Varma A.K., Kwon-Chung K.J.; "Characterization of the glyceraldehyde-3-phosphate of its promoter for heterologous expression in Crypt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
Tremellaceae; Filobasidiella.
NCBI_TaxID=5207;
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Bukaryota; Fungl; Ascomycota; Ascomycota incertae sedis;

Phaeosphaeriaceae; Phaeosphaeria.

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01-OCT-2000 (TYEMBLIEL. 15, Last sequence update)
01-OCT-2000 (TYEMBLIEL. 15, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-B-3501;
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SEQUENCE 337
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-CT-2000 (TrEMBLrel. 15, Last annotation update)
DE GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (GAPDH).
OS Paralichthys olivaceus (Flounder).
OC Eukaryota: Metazoa; Chordata; Creniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Bothidae; Paralichthys.

N NCBI_TaxID-8255;
N [1]
         PORTOR OF THE PO
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Best Local S
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-OCT-2000 (TrEMBLrel. 15, Last annotati
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
GLEGPD.
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Q9UR38;
01-MAY-2000
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INTERPRO IPRO00173; -.

PEAM; PE00044; gpdh; 1.

PRINTS; PR00078; G3PDHDRGNASE.

PROSITE; PS00071; GAPDH; 1.

SEQUENCE 333 AA; 36041 MW;
   Hirano T., Sato T., Okawa K., Kanda K., Yaegashi K., Enei H.; "Isolation and characterization of the glyceraldehyde-3-phosphate dehydrogenase gene of Lentinus edodes."; Biosci. Biotechnol. Biochem. 63:1223-1227(1999). EMBL; AB013136; BAA83550.1; -. EMBL; AB012862; BAA83549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aoki T., Naka H., Katagiri T., Hirono I.;
"Cloning and characterization of glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) cDNA of Japanese flounder, Paralichthys
                                                                                                                                                                                                                                                                      Eukaryota; Fungi;
Tricholomataceae;
                                                                                                                                                                                                                                                                         Lentinula edodes (Shiitake mushroom)
Eukaryota; Fungi; Basidiomycota; Hymw
Tricholomataceae; Lentinula.
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EMBL; AB029337; BAA88
HSSP; P00354; 3GPD.
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                                                                                                                                                                                   SEQUENCE FROM N.A.
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12; Conser
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73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
DEHYDROGENASE (EC 1.2.1.12).
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                                                                                                                                                                                                                                                                                                        Hymenomycetes;
                                                                                                                                                                                                                                                                                                                                 (Lentinus edodes).
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Q9R5J2;
01-MAY-2000
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"Isolation and Characterization of the Gene Encoding Glyceraldehyde-3-
Phosphate Dehydrogenase Of Phaffia rhodozyma";

Submitted (JUN-197) to the EMBL/GenBank/DDBJ databases.

EMBL; AF006483; AAF21599.1; -.

HSSP; P00357; 4GPD.
INTERPRO; IPR000173; -.

PPAM; PP00044; pgbh; 1.

PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.

PROSITE; PS00071; GAPDH; 1.

PROSITE; PS00071; GAPDH; 1.
MEDLINE=92364544; PubMed=1500854;
Pancholi V., Fischetti V.A.;
"A major surface protein on group A streptococci is a
glyceraldehyde-3-phosphate-dehydrogenase with multiple
                                                                                                                                                                                                 Bacteria; Firmicutes; NCBI_TaxID=1301;
                                                                                                                                                                                                                                          Streptococcus.
Bacteria; Firm
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01-MAY-2000 (TrEMBLrel.
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SURFACE DEHYDROGENASE (F
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation updat
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
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INTERPRO; IPRO00173; -.
PFAM; PF00044; 9pdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                      SEQUENCE
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STRAIN-67-385, WILD TYPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phaffia rhodozyma
Eukaryota; Fungi;
Xanthophyllomyces.
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Basidiomycota; Hymenomycetes; Cystofilobasidiales;
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1. 13, Last sequence up
1. 15, Last annotation
(FRAGMENT).
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1; Mismatches
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      binding
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RESULT 13
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Best Local S
Matches 12
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Best Local S
Matches 11
SEQUENCE FROM N.A.

Leutenegger C.M., Mislin C., L

"partial characterization of f

dehydrogenase (GAPDH).";

Submitted (CCT-1998) to the EM

EMBL; AF097177; AAC72840.1; -.

HSSP; P00354; 3GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity.";
J. Exp. Med. 176:415-426(1992).
HSSP; P00361; 1CER.
INTERPRO; IPRO00173; -.
PFAM; PF00044; gpdh; 1.
SEQUENCE 39 AA; 4284 MW; 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097653
097653;
01-MAY-1999
01-MAY-1999
01-OCT-2000
                                                                                                                           O97652 PRELIMINARY; PRT; 76 AA.
097652;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (FRAGMENT)
                                                                                             Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2000 (TrEMBLrel. 15, GLYCERALDEHYDE-3-PHOSPHATE)
                                                                                    NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              EMBL; AF097178; AAC72841.1;
HSSP; P00354; 3GPD.
INTERPRO; IPRO00173; -.
PFAM; PF00044; gpdh; 1.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase (GAPDH).";
Submitted (OCT-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Leutenegger C.M., Mislin C
Partial characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ) C.,
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, Last annotation
DEHYDROGENASE (FI
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3; Mismatches
                     EMBL/GenBank/DDBJ
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                                         Lutz H.
feline
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Pred.
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iion update)
(FRAGMENT).
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                      databases
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Felis.
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity 85.
Matches 12; Conservative
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PFAM; PF00044; 9pdh;
NON_TER 76
NON_TER 76
SEQUENCE 76 AA; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                       041949;
01.NOV-1996 (TrEMBLrel. 01,
01.NOV-1996 (TrEMBLrel. 01,
01.OCT-2000 (TrEMBLrel. 15,
GLYCERALDEHYDE 3-PHOSPHATE E
                                                                                                                                                                                                                                                          Arabidopsis thallana (Mouse-ear cress).

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

RCBI_TaxID=9940;
                              SEQUENCE FROM N.A.
TISSUE-WHOLE SEEDLINGS OF A. THALIANA ECOTYPE COLUMBIA;
TISSUE-T., Amselem J., Chiapello H., Rouze P., Caboche M.,
Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M.,
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z18057; CAA79091.1;
HSSP; P00354; 3GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPC
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Herrmann L.M., Davis W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2000) to the EMBL; AF272837; AAF91410.1;
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| ||||||||||
1 VKVGVNGFGRIGRL 14
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| ||||||||||
3 VKVGVNGFGRIGRL
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106 AA;
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   Arath; GapC; 7185
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; 11612 MW;
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DEHYDROGENASE GAPDH (FRAGMENT).
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Pred. No. 0.06
1; Mismatches
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annotation update)
ROGENASE (FRAGMENT).
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0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gambetti P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
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                                                                                                                                  Hofte H.;
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                                                                                                     SQ FT OR
                                            Query Match
Best Local S
Matches 11
                                                                                                  INTERPRO; IPRO00173; -. PFAM; PF00044; gpdh; 1. Multigene family; Oxidoreductase. NON_TER 87. 87 AA; 10034 MW; ADC
4 VLVGVNGFGRIGR-IGRLVI 22
: :|:||||||| : |:|:
6 IRIGINGFGRIGRLVARVVL 25
                                            l Similarity
11; Conserv
                                            Conservative
                                                      59.1%;
                                            Score 61.5; D
Pred. No. 0.09
6; Mismatches
                                                                                                    ADC06618BA8F5251 CRC64;
                                                       .094;
                                                                 DB 10;
                                              Indels
                                                                  Length
                                                                   87;
                                            1.
                                            Gaps
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Search completed: Job time: 548 sec June 13, 2001, 14:29:47 В

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 13, 2001, 14:27:09; Search time 78.71 Seconds (without alignments) 5.370 Million cell updates/sec
Sequence 1, Appli Sequence 50, Appli Sequence 52, Appli Sequence 2, Appli Sequence 186, App Sequence 6, Appli Patent No. 5290690 Sequence 205, Appli Sequence 2, Appli Sequence 1, Appli Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                            ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-553-110-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-553-110-1
                                     Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08553110
Patent No. 5723301
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOUNT OF THE PROPERTY OF THE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Enghild, Jan
APPLICANT: Strittmatter, Warren J.
TITLE OF INVENTION: Therapeutics for Diseases Associated
TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.U.
STREET: Charlotte
TTY: Charlotte
57233'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Charlotte
STATE: No. 5723301th Carolina
COUNTRY: United States of Ame:
ZIP: 28234
ZIP: 28234
                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Kenneth D. Sibley P.O. Drawer 34009
                                                                                                                                                                                                                     18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burke, James R.
Vance, Jeffrey M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337.55
337.55
337.55
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                                     Conservative
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85.7%;
                                   Pred. No. 0.00
1; .Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-876-941A-16
PCT-US95-13703-18
US-08-259-148A-18
US-08-484-054-18
US-07-876-941A-18
PCT-US95-13703-28
PCT-US95-13703-16
US-08-259-148A-20
US-08-259-148A-20
US-08-680-7803-13703-13
US-08-680-726A-80
US-08-680-726A-80
                                                                                                                                                                                                                                                                                                                             5405-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                   DB 1;
0.0012;
                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                   0;
                                   Gaps
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Result No.

Score

Query Match

Length

BB

SUMMARIES

US-08-553-110-1 US-08-946-026-50 US-08-961-083-54 US-07-928-462-2 US-08-273-247-2 US-08-997-080-186 US-08-997-362-186 US-09-095-855-186 5290690-10

ecore grea and is der

1 US-09-095-855-205 2 US-08-464-073-33 5 5245013-20 1 US-08-678-444-1 4 US-09-007-476-2 1 US-09-007-484-2 2 US-09-007-484-2 3 US-09-007-484-2 3 US-09-007-484-2 3 US-09-222-817-2 3 US-09-222-817-12 3 US-09-222-817-12 4 US-08-259-1488-16 1 US-08-259-1488-16

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4 VLVGVNGFGRIGRI 17

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5290690-11 US-08-903-800A-6 5290690-9

Minimum Maximum

DB BC

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length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

185757 seqs, 19210857 residues

Searched:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Title: Perfect score:

PCT-US01-05825A-31 104

XGLVLVGVNGFGRIGRIGRLVI

2

Run on:

protein -

protein search, using

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model

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued\_Patents\_AA:\*

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2: /cgn2\_6/ptodath3/2

3: /cgn2\_6/ptodath3/2

4: /cgn2\_6/ptodath3/2

5: /cgn2\_6/ptodath3/2

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6: /cgn2\_6/ptodath3/2

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/cgn2\_6/ptodata/2/iaa/BCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

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VKVGVNGFGRIGRL 14

-08-940 Sequence 50, APF-No. 603421

Application US/08946026

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                                                                                                                                                                                                                               RESULT 3
US-08-961-083-54
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                            Sequence 54, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: Y01/4 ....
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/946,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM:
                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                              APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                STATE:
                                                              CITY: Rockville
                                                                              STREET:
                           COUNTRY:
                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                 VLVGVNGFGRIGRI 17
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                 20850
                                              Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                            9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon, Daviel R.
Twardzik, Daniel R.
Mitcham, Jennifer L.
Mitcham, Jennifer L.
MYPOUNDS AND METHODS FOR IMMUNOTHERAPY
MYENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
Dillon, Davin C
                                USA
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                               Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                682-6031
                                                                                                                                              Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                   59.6%;
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    Mismatches

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Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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; TOPOLOGY: 1i; MOLECULE TYPE: US-08-961-083-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
FILING DATE: 19920810

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411

FILING DATE: 16-MAY-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849

FILING DATE: 29-MAR-1989

ATTORNEY, AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Boyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
APPLICANT: von Mering, Gregory O.
Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 19920810
                                                                                                                                                                                                                                                                                                                                         CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LVLVGVNGFGRIGRI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                         32606
                                                                                                                                                                                                                                                                                                                      Gainesville : FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/07928462 5328996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brookes, A.
                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boyle, Michael D.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Diskette, 3.50 inch, 1.4Mb storage HP Vectra 486/33
                                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.6%;
73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anders
                                                                                                                                                                     US/07/928,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62; DB Pred. No. 0.03; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PB340P2
                                                                                                                                                                                                       Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 333;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100

REFERENCE/DOCKET NUMBER:

REGISTRATION NUMBER:

31,794

UF/S&S-13.C2

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MOLECULE TYPE: :-08-273-247-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.0
Best Local Similarity 73.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: UF/S6S-13.C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Applic
Patent No. 613632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 336 amino acids
                                                                                                                                     TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein -928-462-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: Won Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                   TOPOLOGY:
                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                         904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boyle, Michael D.P
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                                     linear
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73.3%;
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Pred. No. 0.032;
3; Mismatches
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RESULT 7
US-08-997-362-186
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                                                                                 Sequence 186, Application US/08997362 Patent No. 5985287
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Best Local Similarity
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Best Local
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NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                     TOPOLOGY: 1, ORD
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
ADDRESSEE: AND OFFICE Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WATSON, APPLICANT: TAN, PAI TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2601 H
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                   3 IRVGVNGFGRIGR 15
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              Skinner, Margot
                           Hiyama, Jun
Visser, Elizabeth
                                                      Tan, Paul
                                                                                                                                                                                                                        Conservative
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Scott, Linda
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                                                                                                                                                                                                                                     56.7%;
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73.3%;
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Pred. No. 0.072;
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Prestidge,

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US-09-095-855-186
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/8/3,9/0 FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997 367
FILING DATE:
                                                                                                                                 NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W.
STREET: 2601 Elliott Avenue, Sui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS NUMBER OF SEQUENCES: 194
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                             TITLE OF INVENTION: Compounds and TITLE OF INVENTION: Treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                               APPLICANT: Visser, Elizabeth APPLICANT: Skinner, Margot
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    APPLICANT: Tan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                            COUNTRY: USA
ZIP: 98121
                                                                                                STATE:
                                                                                                                CITY: Seattle
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5. 6160093
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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84.6%;
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                                                                                                                                   n W. Speckman
Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                           Methods for Diagnosis of Mycobacterial Infections
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;Patent No. 5290690

APPLICANT: MRABET, NADIR;LASTERS, IGNACE;STANSSENS, PATRICK;MATTHYSSENS, GASTON;WODAK, SHOSHANA;QUAX, WILHELMUS J.; TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE;STABILLITY OF PROTEINS
                                                                                                                          RESULT 10
5290690-11
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US-09-095-855-186
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PATENT NO. 5290690

PATENT NADIR: LASTERS, IGNACE: STANSSENS, PATRICK APPLICANT: MRABET, NADIR: LASTERS, IGNACE: STANSSENS, PATRICK MATTHYSSENS, GASTON; WODAK, SHOSHANA; QUAX, WILHELMUS J.

TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE STANDILITY OF PROTEINS

STABILITY OF PROTEINS

UMBBER OF SEQUENCES: 22

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
5290690-10
                                                                                                                                                                                                                                                                                                                                                                     5290690-10
                                                                                                                                                                                                                                                                                                                                                                                                   : FILING DATE: SEQ ID NO:10:
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/705
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/97
NUMBER OF SEQUENCES: 22 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/
FILING DATE: 25-AUG-1989
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 334
                                                                                                                                                                                                      2 VKVGINGFGRIGR 14
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3 IRVGVNGFGRIGR 15
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                                                                                                                                                                                                                                                                                           56.7%;
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- ER: 11000.1002c3
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Pred. No. 0.092;
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US-08-903-800A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08903800A Patent No. 5935789
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SOHN, June APPLICANT: KANG, Hyun APPLICANT: KIM, Hwa-TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RHEE, Sang-Ki
STREET: Keukdong Villa Ka-101, Kwangjang-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CHOI, Eui-Sung
STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
STREET: Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 334
COUNTRY: Republic of Korea ZIP: 120-190
                                                        ADDRESSEE: KIM,
STREET: #3-462,
                                                                                                                                 CITY: Daejeon
                                                                                                                                                STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong. STREET: Seo-gu
                                                                                                                                                                                                                                      CITY: Daejeon
                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                     COUNTRY:
                                                                                                                                                                              ADDRESSEE: KANG, Hyun-Ah
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Shindonga Apt. 2-1101, Yongjeon-dong, Dong-gu
                                                                                                                                                                                                                                                    Nuri Apt. 103-506, Wolpyung-dong, Seo-gu
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CHOI, Eui-Sung
KIM, Chul-Ho
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KANG, Hyun-Ah
KANG, Hyun-Ah
KIM, Hwa-Young
KIM, Hwa-Young
KIM, Hwa-Young
KIM, Hwa-Young
KIM, Hwa-Young
KIM, Hwa-Young
KENTION: AUTONOMOUSLY REPLICATING SEQUENCES,
WENTION: GAPDH GENE AND PROMOTER DERIVED FROM
WENTION: VECTORS CONTAINING SAME AND METHOD FOR
                                                                                                                                                                                                                                                                                                 Republic of Korea
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                                                        Bukahyun-3-dong,
                                                                       Hwa-Young
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RESULT 13
US-09-095-855-205
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5290690-9
;PATEBLE NO. 5290690
; PATEBLE NO. 5290690
; AMATTHYSSENS, GASTON; WODAK, SHOSHANA;QUAX, WILHELMUS J.
;TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE
;STABILITY OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
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Best Local S
Matches 10
              Sequence 205, Application US/09095855 Patent No. 6160093
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                      Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 25-AUG-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 97-3173
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/903,800A FILING DATE: 31-JUL-1997
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les 10; Conserv
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                                                                                                           3 VKVGINGFGRIGR 15
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                                                                                                                                                                                                                                                               LENGTH: 335
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5 VGINGFGRIGRL 16
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2; Mismatches
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0.093;
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APPLICANT:

Visser, Elizabeth

Tan, Paul

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                                                                                                                                                                                                                                      Sequence 33, Application Patent No. 5864028
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 37-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: 'amino acid
STRANDEDNESS; single
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                        APPLICANT: Sloud, Mouldy TITLE OF INVENTION: TNF-1TITLE OF INVENTION: PROTITITLE OF INVENTION: LINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y Match 56.7%;
Local Similarity 84.6%;
nes 11; Conservative
                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-269-0563
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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ZIP: 98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
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                    USA
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linear
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                                                                                                                                                        TNF-ALPHA RIBOZYMES, TNF-ALPHA RIBOZYME BINDING PROTEIN AND DEGRADATION RESISTANT MRNA DERIVATIVLINKED TO TNF-ALPHA RIBOZYMES
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Pred. No. 0.094;
1; Mismatches
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COMPUTER READABLE FORM:

Search completed: June 13, 2001, 14:27:09 Job time: 630 sec

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APPLICATION NUMBER: 6,710
FILING DATE: 30-DEC-1986
APPLICATION NUMBER: 728,8
FILING DATE: 30-APR-1985
SEQ ID NO:20:
LENGTH: 27
                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                        ;Patent No. 5245013
; APPLICANT: Ulevitch, Richard;Tobias, Peter
TITLE OF INVENTION: ACUTE PHASE PROTEIN MODULATING ENDOTOXIC
; ACTIVITY OF LIPOPOLYSACCHARIDES, ASSAY METHODS AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
5245013-20
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATOK AFFECTION UNMBER: PCT/AU/I
PAPPLICATION UMBER: PCT/AU/I
FILING DATE: 03-NOV-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,058
FILING DATE: 03-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.2/
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-391-0525
TELEPHONE: 212-391-0525
TELEPHONE: 212-391-0525
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                  6 VGVNGFGRIGRI 17
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2 IAINGFGRIGRL 13
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                                                             Score 52; DB
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0.0087;
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Title:
Perfect score:
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97
1 EVQLVESGGGLVQPGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390729 seqs, 57163235 residues
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                                                                                                                                                                                                                                                                            /SIDS6/gcgdata/geneseq/yeneseqp/AA1988.DAT:*

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Y50960
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Compugen Ltd
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        Human FVIII antibo
Heavy chain variab
Human immunoglobul
VH domain CDR of a
Human FVIII antibo
Human FVIII antibo
Anti-TNF-alpha ant
Human immunoglobul
Human 5' EST relat
                                                                                                                                                          Description
                                                                                                                                Anti-hIL12 antibod
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## ALIGNMENTS

RESULT

Ħ B40072 Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory; complementarity determining region; CDR; antirheumatic; antiarthritic; antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial; immunosuppressive; Crohn's disease; 24-MAR-2000; 2000WO-US07946 Homo sapiens. multiple sclerosis; Anti-hIL12 antibody H chain V region amino acid sequence 05-FEB-2001 B40072; B40072 standard; Protein; 25-MAR-1999; 28-SEP-2000. WO200056772-A1 (first entry) 99US-0126603 rheumatoid arthritis. 98 ₽

SEQ ID

598.

Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M; Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR; Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL; (BADI ) BASF AG. (GEMY ) GENETICS INST INC.

colon

cancer

This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences B39485-B39516 represent human

anti-IL-12 antibody heavy and light chain complementarity determining

Claim 75;

Page 121; 377pp; English.

disease and multiple sclerosis -

WPI; 2000-638250/61.

New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

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RESULT
Y50960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FVIII antibody A3-C1 scFv heavy chain protein DP-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y50960 standard; Protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                  08-MAY-1998;
                                                                                                                                                                                                                                                                                                                         18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-12 disorders.
                                                                                            WPI; 2000-053102/04
                                                                                                                                                                                                                                                                             07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                    WO9958680-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hemophilia A;
                                                                                                                                                                                   (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l evqlvesggglvqpgrslrl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain; antibody;
scFv; A3-C1.
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                                                                                                                                        Van Den
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor
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                                                                                                                                           Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIII; hemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
6.3e-08;
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Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-G1 specific scFv protein DP-31 which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Fig 9A; 6lpp; English.
                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region of murine antibody ldfb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R52053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R52053 standard; Protein; 117
                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                            modelling; surface residue; modify.
                                                                                                                                                                                                                                                                                                                                                                                                 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1996
          WPI; 1994-120230/15
                               Guild BC,
                                                                                     09-SEP-1992;
                                                                                                           07-SEP-1993;
                                                                                                                                 13-APR-1994
                                                                                                                                                       EP592106-A1.
                                                                                                                                                                                     Region
                                                                                                                                                                                                          Region
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                                                    (PEDE/) PEDERSEN J T. (IMMU-) IMMUNOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                humanised; murine; human; heavy chain; light; variable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                               Pedersen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                      92US-0942245
                                                                                                           93EP-0307051
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                             /label- CDR_:
                                                                                                                                                                                                                                          /label= FR_2
                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                /label= framework_region_1
/note= "FR 1"
                                                                                                                                                                                                                     'label- CDR_2
                                                                                                                                                                                                                                                                          'label = complementarity_determining_region_1
                                                                                                                                                                                                label- FR_3
                                                                                                                                                                                                                                                                                                                                                                                       complementarity determining
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Pred. No. 6.4
0; Mismatches
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                               Roguska MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4e-08;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                       region;
                                 Searle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 99;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the heavy chain variable (LC VR) region of murine antibody ldfb. This sequence was aligned with 11 other known antibody LC VRs and a set of framework positions of surface exposed amino acid residues was determined. This information can be used in a method to determine how to modify a rodent antibody or fragment by resurfacing in order to produce a humanised rodent antibody. Residues (determined from alignment) at positions 118, 120, 122, 126, 127, 128, 130, 131, 133, 135, 145, 160, 161, 162, 183, 184, 186, 187, 195, 196, 197, 208, 209, 210, 212 (numbered from the N-terminal of the complete heavy chain) are accessible residues. None of the entire combinations of surface residues in the murine sequences were found in the human sequences and vice versa.
                                                                                                                                                                     DNA fragment comprising human immun production of human immunoglobulin
sequences encoded by novel isolated genes. The genes (Q78939-79002) were solated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1995 (first entry)
                                                                                                         Protein sequences
                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R66337 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved
                                                                                                                                                                                                                                                                                                                                                  10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         However the residues in individual positions appear to be conserved.
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                                                                                                                                         56; Page 94-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin
                                                                                                                                                                                                                              Q78987.
                                                                                                                                                                                                                                                                                                                JAPAN TOBACCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                             Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                  93WO-JP00603
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                                                                                                   (R66295-51) are novel human immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable
                                                                                                                                     130pp;
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                                                                                                                                                                         human immunoglobulin Vh
unoglobulin in mammalian
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                                                                                                                                         Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin; variable; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 15;
Pred. No. 7.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #43.
                                                                                                                                                                         genes
hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Best Local
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                                                                                                                                This sequence represents a VH domain complementarity determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0x10^-8M for estradiol, and a dissociation constant of at least 500-fold higher for the steroid hormones selected from estriol,
            used for monitoring estradiol levels, e.g. during the menstrual cycle, hormone replacement therapy and for diagnosing oestrogen secreting tumours. The sbps can provide for discrimination between estradiol and
                                                              testosterone, dihýdrotestosterone, progesterone, estriol-3-sulphate estriol 3-beta-di-glucuronide, where the polypeptide comprises an antibody vH domain. The spbs can be used in an immunoassay for determining the presence or absence of estradiol in a sample. They contains the presence or absence of estradiol in a sample.
                                                                                                                                                                                                                                                               Claim 1; Column 25-26;
                                                                                                                                                                                                                                                                                                       New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacement thereney and for dispension pastrones especially themselves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         menstrual cycle; horn diagnosis; VH domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Estradiol; complementarity determining region; CDR; estriol-3-sul antibody antigen binding domain; steroid hormone; estriol; testos dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                digested with TaqI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5977319-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VH domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y43255
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 evqlvesggglvqpgrslrl
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DB; Z31653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of anti-estradiol antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0028897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0958201
                                                                                                                                                                                                                                                                                              diagnosing oestrogen secreting tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone replacement therapy; oestrogen secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                           26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         Pritchard
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Pred. No. 7.8e-08;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; estriol-3-sulphate; estriol; testosterone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local :
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                                                                               Matches
                                                                                                                                  Sequence
                                                                                                                                                            hybridizable polynucleotides) comprising a contiguous nucleotide sequent coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein B35 which is used
                                                                                                                                                                                                                                                This invention
                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                               Voorberg JJ,
                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FVIII antibody A3-C1 scFv heavy chain protein B35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y50963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                 Example 8; Fig
                                                                                                                                                                                                                                                                                                                                                                   (SANQ-)
                                                                                                                                                      factor VIII antibody A3-C1 spec
in the method of the invention.
                                                                                        Local Similarity
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                                      evqlvesggglvqpgrslrl 20
                                                          EVQLVESGGGLVQPGRSLRL 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                  120 AA;
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                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain;
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                                                                                                                                                                                                                                                                                                                                                 Van Den
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCFV;
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                                                                                                                                                                                                                                                                 9A; 61pp;
                                                                                                                                                                                                                                                describes
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                                                                                                                                                                                                                                                                                                                                                                                                             99WO-NL00285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody;
A3-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                 Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                              a novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 97; DB zv;
Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                        Score 97; DB 21; Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor VIII;
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                 Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                  Length 120;
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                                                                                Gaps
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilla A patients. This sequence represents a fragment of the human factor VIII antibody heavy than variable region protein B35 of the invention of the human factor VIII antibody heavy than variable region protein B35 of the first sequence of the protein B35 of the human factor VIII antibody heavy than variable region protein B35 of the first sequence of the protein B35 of the first sequence of the protein B35 of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies \cdot
malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Fig 9D; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heavy
hemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human FVIII antibody heavy chain variable
                                                                                   Human; tumour necrosis factor-alpha; TNF-
heavy chain; variable region; inhibition;
                                                                                                                                                           Anti-TNF-alpha antibody heavy chain variable region.
                                                                                                                                                                                                           19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-053102/04.
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                                                                treatment; sepsis; disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                                     standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain; antibody; factor VIII; hemostatic;
                                                                                                                                                                                                           (first entry)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97;
                                                                                                                TNF-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region. B35 protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0:
                                                                     infectious
                                                                                                                  antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
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                                                                     disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, ostcoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a novel anti-human tumour necrosis factor alpha (TNF-alpha) antibody (Ab) heavy chain variable region. The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, Theumatoid autoimmune diseases, e.g. rheumatoid arthritis, Theumatoid
  Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
                                      Human immunoglobulin variable heavy chain #9
                                                                                 02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 76; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-415302/38.
N-PSDB; T88404.
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Salfeld JG, Schoenhaut D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-1997;
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                                                                                                                                                           R66303 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
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JA, McGuiness BT, Roberts AJ, Sakorafas
, Schoenhaut D, Vaughan TJ, White M, W.
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llarity 100.0%;
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96US-0599226
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                                                                                                                                                                                                                                                                                                                                    Score 97; DE Pred. No. 8e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on human umbilical vein
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Wilton
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  09-APR-1999;
                                                                                                                                                                                                                                                       Human 5' EST related polypeptide SEQ ID
                                                                                                                                                                                                                                                                                                01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                        21-OCT-1999
                                                                               WO9953051-A2
                                                                                                                  Homo sapiens
                                                                                                                                                         regulation;
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                                                                                                                                                                                                                                                                                                                                                                           Y64737 standard; Protein; 149
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                                                                                                                                                           identification
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  99WO-IB00712
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cosmid; placenta; vector; pJB81; E.coli; mammalian.
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DNA fragment comprising human immunoglobulin Vh production of human immunoglobulin in mammalian genes hosts for

Protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q7839-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers (Q78917-38. The genes are subdivided into 5 families of vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placents. The DNA was partially digested with TagI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pB881. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.

red. No. 8.1 8.1e-08; thes 0; DB 16; Length 123; Indels 0 0;

NO:898.

Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc sequences, corresponding to human secreted proteins. Y6451 to Y65438 C represent the EST-related proteins corresponding to Z42265 to Z43052. CC The 5° ESTs can be used for producing secreted human gene products. CC They can be used to identify and isolate 5' untranslated regions (UTRs) CC and upstream regulatory regions which control the location, development CC stage, rate, and quantity of protein synthesis, as well as stability of control the location, development CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to CC procedures to identify individuals, or in diagnostic procedures to CC identify individuals having genetic diseases resulting from abnormal CC The nucleic acids encoding signal peptides can be used for directing CC extracellular secretion of a polypeptide or the insertion of a cell. The proteins encoded by the EST sequences may be useful in treating a CC variety of human conditions. Secreted proteins have therapeutic value, CC and the identification of new secreted proteins is valuable. Z42249 to CC 242264 and Y66404 to Y66650 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                21-SEP-2000
                                                 WO200055351-A1
                                                                                                                                                            identification; cytostatic; cardioactive; neuroprotective; vulnerary;
immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                   infectious disease;
                                                                                                                             neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder,
                                                                                                                                                                                                                                                      Human colon cancer antigen protein sequence SEQ ID NO:1187
                                                                                                                                                                                                                                                                                           09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 B53647 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        z42265 to z43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. x64651 to x65438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 627; 837pp; English.
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28-APR-1998;
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                                                                                                                                                                                                                     colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 AA;
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98US-0069047,
                                                                                                                cardiovascular
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Pred. No.
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                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                     complementarity determining
                                                                                                                                                                                                                                                     Plasmid
                                                                                                                                                                                                                                                                                Recombinant sc3D6 anti-HIV gp160 antibody.
                                                                                                                                                                                                                                                                                                                     25-MAR-1992
                                                                                                                                                                                                                                                                                                                                                    R20059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C97991 to C98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in B53234 to B54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                             R20059 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 1767-1768; 2104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-587534/55
N-PSDB; C98404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification
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                                                                                                                                                                                                                                                  pUC3D6LC; PUC3D6HC; human immunodeficiency virus; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                 (first entry)
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/label= Framework_3_heavy_chain
100..116
                                                                                                   /label= CDR_1_heavy_chain
                                                                                                                                      /label= Framework_1_heavy_chain
                                                                                                                                                                       Location/Qualifiers
                                           label= CDR_2_heavy_chain
                                                                       label= Framework_2_heavy_chain
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Matches 20
  Plasmid pUC3D6HC; human immunodeficiency virus; AIDS; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cell line 3D6 (87110301; Porton Down) produces a MAb of the IgG1/Kappa type that reacts specifically with HIV-1 gp41 and also weakly cross-reacts with HIV-1 gp120. Gene construct sc3D6 was engineered using the variable region coding regions of the heavy and light chains of antibody 3D6, joined by a linker. The recombinant protein binds to HIV gp160. See also Q20066 and Q20067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09118983-A.
                                                                                                                                         25-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                   Heavy chain of 3D6 anti-HIV antibody.
                                                                                                                                                                                                                                         R20057 standard; Protein; 475
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                                                                                                                                                                                                                                                                                                                                                                  1992-007468/01.
DB; Q20068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 100.0%; similarity 100.0%; 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 AA;
                                                                                                                                      (first entry)
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177..191
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243..253
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236..242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 97; DB 13;
Pred. No. 1.7e-07;
Mismatches 0;
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                                                                                                                                                                                                                                                                    RESULT
Human; immune system associated protein; HISAP-5;
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Query Match
Best Local S
Matches 20
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See also Q20067 and Q20068.
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 24; 52pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-007468/01.
                             Human immune system associated protein HISAP-5.
                                                           15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felgenhauer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUNG/) JUNGBAUER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1990;
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                                                                                                                                                                                                           1 EVQLVESGGGLVQPGRSLRL
                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                 475
                                                                                                                                                                                                                                                           Conservative
                                                           (first entry)
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l..19
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20..49
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.18..134
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                                                                                                                                                                                                                                                                       Score 97; DB 13; Pred. No. 3.5e-07;
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                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                    Length 475;
immune disorder;
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RESULT 15
R97323
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Best Local Similarity
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(IMMU-) IMMUNOMEDICS INC.
                                  05-OCT-1994;
                                                                                                                        W09611013-A1
                                                             28-SEP-1995;
                                                                                            18-APR-1996
                                                                                                                                                                                  Monoclonal antibody; humanised; mouse; framework region; FR; CDR; complementary determining region; anti-carcinoembryonic antigen; CEA; diagnosis; imaging; therapy; immune response.
                                                                                                                                                                                                                                      Humanised monoclonal antibody heavy chain framework region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atheroscierosis, Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                               15-OCT-1996
                                                                                                                                                                                                                                                                                                              R97323;
                                                                                                                                                                                                                                                                                                                                   R97323 standard; peptide; 30 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Yue H, Lal P, Hillman JL, Au-Young J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative 0;
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                                94US-0318157.
                                                            95WO-US11964.
                                                                                                                                                                               imaging; therapy; immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 22;
Pred. No. 3.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 483;
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Search completed: June 13, Job time: 670 sec
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                                                                                                                                                                                                                                                                                       Complementary determining regions (CDRs) of a parental murine class complementary determining regions (CDRs) of a parental murine class III anti-carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a heterologous antibody which can be derived from C any species including human, retain the anti-CEA binding specificity of the parental murine MAb but are less immunogenic in a human C subject than the parental MAb. The humanised antibodies can be used in diagnosis, imaging and therapy of CEA-producing cancers and C patients receiving the humanised antibodies and conjugates show improved therapeutic results, decreased immune responses and decreased immune responses and confused immune responses and the decreased immune responses and confused. This sequence corresponds to the first framework region of the heavy chain of the humanised MAb. See R97313-97333.
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 39; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanised anti-CEA monoclonal antibody - having engrafted murine CDRs, used for diagnosis, imaging and therapy of CEA-producing
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                                                                                                             1 EVQLVESGGGLVQPGRSLRL 20
                                                                                          1 evqlvesgggvvqpgrslrl 20
                                                                                                                                                                                                                                                                     30 AA;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hansen HJ;
                                                                                                                                                                                    96.98;
95.08;
              2001, 14:25:51
                                                                                                                                                                                Score 94; DB 17; Length 30; Pred. No. 5.2e-08;
                                                                                                                                                                  Mismatches
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Minimum
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primand is derived by analysis of the total score distribution.
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## ALIGNMENTS

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Ig heavy chain V region (DP-31) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26927
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o A;Reference number: S26885; MUID:93021117
A;Accession: S26927
                                                                                                                                 A;Cross-references: EMBL:X73605; NID:g509797; PIDN:CAA51998.1; PID:g509798 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                 R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune re A;Reference number: S69896; MUID:93272805
A;Accession: S69896
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (clone RFKL5H), rheumatoid factor - human C;Species: Homo sapiens (man) C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999 C;Accession: S69896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12333; NID:g32885; PIDN:CAA78203.1; PID:g32886
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-100 < RAN>
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20; Conservative (
100.0%; Score 97; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No. 4.5e-08;
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Best Local Similarity Matches 20; Conserv

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4.6e-08;

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RESULT 3
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Ig heavy chain - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Accession: S31118
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Scl Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third of A; Reference number: S31104; MUID:92111633
A; Accession: S31118
A; Accession: S31119
A; Accession: S31119
                      Ig heavy chain V region - human C; Species: Homo sapiens (man) C; Date: 06-Jan-1995 *sequence_revision C; Accession: S30532 R; Mariette, X.
                                                                                                                      RESULT
S30532
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R;Rabphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.;
Eur. J. Immunol. 22, 247-251, 1992
A;Tille: Restricted utilization of germ-line V(H)3 genes and shor A;Reference number: S31104; MUID:92111633
A;Accession: S31104
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A; Residues: 1-121 < RAA>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 5.
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  October 1992
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                                                 06-Jan-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                          BB
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                      Query Match
Best Local Similarity
          Matches
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A; Molecule type: mRNA
A; Residues: 1-145 <FEL>
A; Residues: 1-145 <FEL>
A; Cross-references: EMBL:x53613; NID:g23865; PIDN:CAA37675.1; PID:g762936
C; Superfamily: Immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                        R;Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A;Title: Nucleotide sequences of the cDNAs encoding
A;Reference number: S11239; MUID:90370490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-128 <CUI>
A; Residues: 1-128 <CUII-
A; Cross-references: EMBL: 214171; NID: g31007; PIDN: CAA78540.1; PID: g31008
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 23-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                            C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change C;Accession: S11239
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                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
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A;Accession: S31595
A;Accession: S31595
A;Status: preliminary
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C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; I submitted to the EMBL Data Library, June 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: EMBL;Z18318
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin c;Keywords: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-123 <MAR>
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A; Accession: S30532
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Pred. No. 5.9e-08;
Pred. No. 5.9e-08;
Score 97; DB 2;
Pred. No. 6.7e-08;
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5.6e-08;
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Conservative

0;

Mismatches

Length 145

0,

Gaps

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Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S44115
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma :rescue of vaccense number: S44105
A:Reference number: S44105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <HAW>
A:Cross-references: EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PID:g940526
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
anti-SS-A/Ro 60K peptide heavy chain E-56 - human (fragment) C;Species: Homo sapiens (man) C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000 C;Accession: PC4281 R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H. Blochem. Biophys. Res. Commun. 232, 101-106, 1997 A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from A;Reference number: PC4279; MUID:97236289 A;Accession: PC4281
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S46390
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PC4281
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A;Molecule type: DNA
A;Residues: 1-114 <FIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision
C:Accession: $46390
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Pred. No. 1.5e-07;
1; Mismatches 0;
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A; Molecule type: protein
A; Residues: 1-123 <SUZ>
C; Comment: This antibody is commonly found in systemic
C; Superfamily: immunoglobulin V region; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                        A;Experimental source: B cells from patient AW with acute lymphoblastic l A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA R;Tomilnson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fi A;Reference number: S26885; MUID:93021117
A;Accession: S26892
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       CiSpecies: Homo sapiens (man)
C;Date: 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PLOII6; 826892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
J. Exp. Med. 168, 229-245, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: B cells from patient TD with acute lymphoblastic l A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin F;31-35/Region: complementarity-determining 1 F;49-65/Region: complementarity-determining 2
A;Cross-references: EMBL:212349; NID:g32918; PIDN:CAA78219.1; PID:g32919 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
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C:Date: 07-Jun-1990 #sequence_revision
C:Accession: PL0120
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PL0120
                                                                                    A; Molecule type: DNA
A; Residues: 1-98 < TOM>
                                                                                                                                                                                                                                                                                                            A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
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A; Residues: 1-94 <BIR>
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Pred. No. 1.6e
1; Mismatches
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C; Keywords: hete F; 15-98/Domain:
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C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-113 <MAR>
                                                                                                                                                                                                                                         A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38488
A;Accession: S38490
                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                     h;Status: preliminary
                                                                                                                                                                                                                                                                                                       R; Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID:g32913 A;Note: designated DP-46
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:217394; NID:g32843; PIDN:CAA78997.1; PID:g32844
A;Note: designated COS-8
R;Pomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117
A;Reference number: S26885; MUID:93021117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G. submitted to the EMBL Data Library, October 1992
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A;Residues: 1-98 <TOM>
                                                                                                  ;Cross-references: EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; PID:g414028; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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Score 91; DB 2;
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Search completed: June 13, 2001, Job time: 744 sec
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A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neur
A;Reference number: S57408
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A;Molecule type: mRNA
A;Residues: 1-113 <PAT>
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C;Date: 10-Oct_1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
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PIR; A02055; G1HUKL.
PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND DISULFIDE BONDS.
MEDILINE-83289131; Pubmed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies.
structure of crystallized monoclonal immunoglobulin IgG1
structure of crystallized monoclonal immunoglobulin IgG1
hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                          Marquart M., Deisenbofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment at and 1.0-A resolution.";
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Eukaryota; Metazoa; (
Mammalia; Eutheria; |
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MEDLINE-81072295; PubMed-7441755;
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RESULT 3
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HOMO Saplens (Human).

Homo saplens (Human).

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P01777;
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IG HEAVY CHAIN V-III REGION TEI.
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  MEDLINE-74142702;
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15-JUL-1999 (Rel. 38, Last annote
16 HEAVY CHAIN V-III REGION GAL.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2
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HSSP; P01772; 2IG2.
InterPro; IPR003006; -.
Pfam; PP00047; 1g; 1.
Inmunoglobulin V region.
In TER 119 AA; 12802 MW; 7
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Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and individual patient. III. The complete amino acid region of the IgM paraprotein."
Immunochemistry 13:995-999(1976).
-i- MISCELLANEOUS; THIS CHAIN WAS OBTAINED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA O
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Pfam; PF00047; ig; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
Proc. NISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM
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"Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain
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MEDLINE-88144476; PubMed-3125551;
Wilson M.R., Middleton D., Warr G
"Immunoglobulin heavy chain variationships of two of two of the control of the c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eatinopterygii; Neopterygii; Teleostei; Euteleostei; Cypriniformes; Cyprinidae; Cyprininae; Carassius.
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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 5A PRECURSOR.
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; Primates;
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n variable region
f two genes and a
                                                        IG HEAVY CHAIN V REGION 5A.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
BY SIMILARITY.
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Pred. No. 2.5e-07
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   9C2279E2DF199B12 CRC64;
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RESULT 8
HV3I_HUMAN
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Best Local S
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Best Local
                               SEQUENCE.

MEDLINE-77070269; PubMed-wzb,,,

Ponstingl H., Hilschmann N.;

Ponstingl H., Hilschmann N.;

The rule of antibody structure. The primary structure of monoclonal IgGl immunoglobulin (myeloma protein Nie). I? chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure.";

peptides and discussion. Chem. 357:1571-1604(1976).
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InterPro; IPR003006; -
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
NON_TER 118 118
SEQUENCE 118 AA; 13087 MW;
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HV3V_HUMAN STAN
P80419;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
15-JUL-1999 (Rel. 3
MEDLINE=77070267; PubMed=1002129; Dreker L., Schwarz J., Reichel W., "Rule of antibody structure. The p
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Mammalia; Eutheria;
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IG HEAVY CHAIN V-III REGION NIE
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HEAVY CHAIN V-III REGION GAR.
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Primates;
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Pred.
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primary structure
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RESULT 10
HV3R_HUMAN
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AC P01779
DT 21-JUL
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            HV3R_HUMAN
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InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
NON_TER 115 115
SEQUENCE 115 AA; 12356
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21-JUL-1986 (Rel. 01, Created)
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15-JUL-1999 (Rel. 38, Last and
IG HEAVY CHAIN V-III REGION T:
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Immunoglobulin V region
MOD_RES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P01772; 2IG2.
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PIR; A02047; H3HU26.
InterPro; IPR003006; -
Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Si
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Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR: A02062; A1HUTU.
InterPro: IPR003006; -.
                                             SIGNAL
                                                                                                                                                                                                                             Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
                                                                                                                                                                                                                                                                                               MEDLINE=81101090; PubMed=6450418;
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                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV3C_HUMAN
P01764;
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MEDITINE-74142702; PubMed=4522793;

Capra J.D., Kehoe J.M.;

"Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ofam; PF00047; 1g; 1.
Immunoglobulin V region.
116 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A.
-i- MISCELLANEOUS: THIS CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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      117
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      ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
     12582
                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                    Signal.
    WW;
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                      IG HEAVY CHAIN V-III REGION VH26
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Pred. No. 7.26
1; Mismatches
E826733F1A3CB0F1 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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WAS ISOLATED FROM
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7.2e-07;
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Query Match

Score

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RESULT 13
HV3M_HMAN
ID HV3M_H
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D7 21-JUL
D7 21-JUL
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D7 15-JUL
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HV30_HUMAN
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Best Local :
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Matches 18; Conserv
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
NON_TER 117 117
                                                                   SEQUENCE.

MEDILINE-75046755; PubMed-4139708;

Capra J.D., Kehoe J.M.;

Capra J.D., Kehoe J.M.;

Structure of antibodies with shared idiotypy: the complete of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANT GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                             HV3M_HUMAN STANDARD; PRT; 119 AA P01774; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 16 HEAVY CHAIN V-III REGION POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-74142702; PubMed-4522793;
Capra J.D., Kehoe J.M.;
"Variable region sequences of five human immunoglobulin of the VH3 subgroup: definitive identification of four h hypervariable regions.";
Proc. Natl. Acad. Sci. U.S. A. 71:845-848(1974).
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                      PIR; A02057; M3HUPM. HSSP; P01772; 2IG2.
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Mammalia; Eutheria; Primates; Catarrhini;
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1-JUL-1986 (Rel. 01, Last sequence up
5-JUL-1999 (Rel. 38, Last annotation
G HEAVY CHAIN V-III REGION WAS
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117 AA;
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InterPro; IPRO03006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 115 115
SEQUENCE 115 AA; 12379 MW; :
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Immunoglobulin V
VARIANT 54
                                                                                                                                                                                                                                                                 _MOUSE
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SEQUENCE.

MEDLINE-80049769; PubMed-115869;
Robinson E.A., Appella E.;
"Amino acid sequence of a mouse
                                                                                                                                                                        HV17_MOUSE STANDARD; PRT; 117 AA. P01786; P01786; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION MOPC 47A.
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SEQUENCE
                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V-III REGION BUT.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                a mouse myeloma
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                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Ogy509 homo sapien
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Ogy166 rattus sp.
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Ogy167 mus musculu
Oguc53 homo sapien
Ogul73 homo sapien
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Ogul75 homo sapien
Ogul76 homo sapien
Ogul776 homo sapien
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44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.8	45.4	45.4	45.4	45.4	46.4	46.4	46.4	46.4	47.4	48.5	50.5	51.5	52.6	54.6	55.7	55.7	55.7
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Q73312	Q73310	Q73309	Q9KWF1	035444	Q9LT89	Q9X7Q1	Q9S2V7	Q9Y3R3	Q9VUB6	Q92547	Q9UEB9	065709	Q9NZQ2	Q9UPX3	023154	Q9VBU5	Q9L0S6	Q9ZAF0	Q9Y298	095978	Q9Z1C6	095973	Q9UL75	Q9QXE9	Q9QXF0
Q73312 human immun	Q73310 human immun	Q73309 human immun	Q9kwf1 pseudomonas	O35444 mus musculu	Q91t89 arabidopsis	· Q9x7q1 streptomyce		Q9y3r3 homo sapien		Q92547 homo sapien	Q9ueb9 homo sapien	065709 arabidopsis	Q9nzq2 homo sapien	Q9upx3 homo sapien	O23154 arabidopsis	Q9vbu5 drosophila	Q910s6 streptomyce	ther		-	Q9z1c6 mus musculu		Q9ul75 homo sapien	Q9qxe9 mus musculu	Q9qxf0 mus musculu

## ALIGNMENTS

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Q9UL84;
Q1-MAY-2000 (TrembLrel. 13, Created)
Q1-MAY-2000 (TrembLrel. 13, Last sequence update)
Q1-OCT-2000 (TrembLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;

"Myosin-reactive autoantibodies in rheumatic carditis and normal
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EMBL; AFO35030; AAD56266.1; -.
HSSEP P01772; ZFB4.
INTERPRO, IPR003006; -.
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122 AA;
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Young D.C.
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O9UL72;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
HOMO Saplens (Human).
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                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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MCBI_TaxID=9606;
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118 AA;
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2e-06;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2000 (TrEMBLrel. 14, Last anno
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY
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01-JUN-2000 (Trembirel. 14, Last annotation update)
MYOSIN REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
HOMO Sapiens (Human).
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MEDLINE-98277139; PubMed-9614934;
Van der Merwe P.L.,
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O9UL93; O1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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INTERPRO; IPR003006;
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n der Merwe P.L.,
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                                                                           Score 87; DB pred. No. 5.4e
1; Mismatches
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annotation update)
EAVY CHAIN VARIABLE
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity 90.0
Matches 18; Conservative
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Q9UL71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                  INTERPRO; IPRO03006;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
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                                                                                                                                                                                                                                               PFAM; PF00047;
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131 AA;
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Catarrhini; Hominidae;
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01-MAY-2000
01-MAY-2000
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01-NOV-1999
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VH3 PROTEIN
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SEQUENCE
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"Human VH gene sequence.";
"Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035268; BAA87067.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96071149; PubMed=7475288;
Cao J., Vesclo R.A., Rettig M.B.,
Lichtenstein A.K., Berenson J.R.,
"A CD10-positive subset of maligna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y509;
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Mammalia; Eutheria;
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Mammalia; !
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last anotation updat.
IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
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Metazoa; Chordata; C
Metazoa; Primates; (
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                                                                    Conservative
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Last annotation updat
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                                                                                         7.4e-05
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2.9e-05;
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Matches 15
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Best Local Similarity
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SEQUENCE
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"Cloning of cDNAs encoding for
antibody (Mab 7, its light and
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                             single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; -
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                PFAM; PF00047; ig;
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Cohen H., Cohen O., Gagnon J.;
Coren prolactin binding protein (PRL-BP) of human
identified as IgG.",
C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
HSSP; P01789; IMCP.
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TYEMBLEEL 13, Created)
01-MAY-2000 (TYEMBLEEL 13, Last sequence update)
01-CCT-2000 (TYEMBLEEL 15, Last annotation updat
PROLACTIN-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR003006; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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nes 15; Conserv
                            2 VQLVESGGGLVQPGRSLRL
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VQLQESGGGLVKPGGSLKL
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encoding for anti-white pir
ts light and heavy chains)
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                                                                                        Score 72; DB Pred. No. 0.00 2; Mismatches
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Pred. No.
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Sciurognathi; Muridae;
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                                                                                                               DB 11;
0.0046;
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pine blister rust monoclonal
ns) and construction of a
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; Murinae; Mus
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Q9UC53;
01-MAY-2000
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Q9QYF0;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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STRAIN-BALE/C; TISSUE-SPLEER,
shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
"Isolation of a novel type of vascular cell wall-specific monoclonal
"Isolation of a novel type of vascular cell wall-specific monoclonal
"Isolation of a novel type of vascular cell wall-specific monoclonal
                                                                                                 MEDIJINE-96033130; PubMed-8582963; Shiraishi Y., Yamamoto D., Hasegawa T Shiraishi Y., Yamamoto D., Hasegawa T Miki S., Tanaka T., Suzuki T., Soma H.; "Diagnostic relevance of abortion-associated human expressed on the cell surface of tumour promoter-tr syndrome cells.", Edward Company Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB036341; BAA88633
HSSP; P01607; 1REI.
INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 2.
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STEQUENCE FROM N.A.
STEQUENCE FROM TISSUE SPLEEN;
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STRAIN=BALB/C; TISSUI
Shinohara N., Demura
Submitted (DEC-1999)
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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
77 KDA SPONTANEOUS RECURRENT ABORTION-ASSOCIATED HU
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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    Local Similarity 93. 
les 14; Conservative
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40 QVKLQQSGGGLVKPGGSLKL
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Metazoa; Chordata; C
-··heria; Rodentia; !
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AA; 31867 MW;
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                       68.0%;
93.3%;
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65.0%;
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to the EMBL/GenBank/DDBJ databases.
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i; Hominidae; Homo.
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RESULT 15
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                                                                                                                Query Match 60.8%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Rader C., Ritter G., Nathan S., Elia M., Gout I., Jungbluth A.A.,

Cohen L.S., Welt S., Old L.J., Barbas C.F. III.;

"The rabbit antibody repertoire as a novel source for the generation

of therapeutic human antibodies.";

J. Biol. Chem. 275:13668-13676 (2000).

EMBL: AF245501; AAF68448.1; ...
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-HUMAN A33 HEAVY CHAIN DOMAIN (FRAGMENT).
0ryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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RADER C., Ritter G., Nathan S., Elia M., Gout I., Jungbluth A.A.,

Cohen L.S., Welt S., Old L.J., Barbas C.F. III.;

"The rabbit antibody repertoire as a novel source for the generation

of therapeutic human antibodies.";

J. Biol. Chem. 275:11368-11676 (2000).

EMBL, AF245503; AAF68450.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLR) 15, Last annotation update)
ANTI-HUMAN A33 HEAVY CHAIN DOMAIN (FRAGMENT).
0ryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9N0W6;
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3 QLVESGGGLVTLGGSLKL
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|QLMESGGGLVTLGGSLKL
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124 AA;
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124 AA;
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13508 MW;
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                                                                                                                Score 59; DB 6 Pred. No. 0.11; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 6; Length 124; Pred. No. 0.039;
                                                                                                                                                                                                                                                                   96C9B29FE26724C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96D2B29FE27C24C8 CRC64;
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Search completed: Job time: 548 sec

June 13,

2001,

14:29:47

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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match Length
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97
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/Packfiles1.pep:*
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     US-07-942-245-24
US-08-545-809A-131
US-08-476-809A-131
US-08-476-809A-131
US-08-476-39-9
US-08-476-349A-9
US-08-476-349A-9
US-08-476-349A-9
US-08-476-349A-9
US-08-478-349A-9
US-08-652-558-3
US-08-652-558-3
US-08-652-558-46
US-08-652-558-46
US-08-652-558-46
US-08-652-558-46
US-08-652-558-46
US-08-652-558-3
US-08-652-558-46
US-08-652-558-46
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US-08-652-558-46
US-08-652-558-3
US-08-859-649-23
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Sequence 24, Appl Sequence 97, Appl Sequence 98, Appl Sequence 99, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 99, Appl Sequence 30, Appl Sequence 31, Appl Sequence 34, Appl Sequence 44, Appl Sequence 45, Appl Sequence 46, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 11, Appl Sequence 11,
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US-07-942-245-24
                                                                                                                                              Query Match
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Matches 20
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Patent No. 5
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Result

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91	91	91	91	91	92	93	93	94	94	94	94	94	94	94	94	94	94
93.8	93.8	93.8	93.8	93.8	94.8	95.9	95.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9
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US-08-545-809A-115	US-07-942-245-36	US-07-942-245-18	US-08-211-202-141	US-08-211-202-118	US-08-958-201-8	US-08-309-025-3	US-08-320-515B-3	PCT-US95-11405-35	US-08-661-052-4	US-08-318-157B-7	US-08-599-226-10	PCT-US94-07659-6	US-09-266-119-22	US-08-760-840A-22	US-08-318-157B-58	US-08-318-157B-17	US-08-318-157B-15
Sequence 115, App		Sequence 18, Appl	Sequence 141, App	Sequence 118, App	Sequence 8, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 35, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 10, Appl	Sequence 6, Appli	Sequence 22, Appl	Sequence 22, Appl	Sequence 58, Appl	Sequence 17, Appl	Sequence 15, Appl

## ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-942-245-24
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SEARLE, Ant APPLICANT: REES, Ant APPLICANT: ROUSKA, Mic APPLICANT: GUILD, BraTITLE OF INVENTION: SURE TITLE OF INVENTION: ANTINUMBER OF SEQUENCES: 527 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2100 Pens
CITY: Washington
STATE: D.C.
COUNTRY: United S
                   1 EVQLVESGGGLVQPGRSLRL 20
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EVQLVESGGGLVQPGRSLRL
                                                                  Similarity 100.
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stephen M.J.

SKA, Michael A.

SKA, Michael A.

N: Braydon C.

N: SURFACE RESIDUE VENEERING OF RODENT

SS: 522
                                                                              100.0%;
                                                                  0;
                                                                                  Score 97; [
Pred. No. 5.
                                                                  Mismatches
                                                                                                   DB 1;
                                                                  .4e-08;
                                                                                                Length 117;
                                                                  Indels
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Gaps

Diskette

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US-08-545-809A-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-545-809A-97
                                                                                                                                                                                                                   Patent No
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
                                                                                   APPLICANT: HONJO, TASUKU
APPLICANT: MAISUGA, FUNIÀNIKO
APPLICANT: MAISUGA, FUNIÀNIKO
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TAVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                 STATE: MA
COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                STATE:
                                                         CITY: Boston
                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                 20 EVQLVESGGGLVQPGRSLRL 39
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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CITY: Boston
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                                                                                                                                                                                                                131, Application US/08545809A
o. 6096878
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19968
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CANT: Honjo, Tasuku
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                                                                        225 Franklin Street
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225 Franklin Street
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10-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 97; 100.0%; Pred. No.
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
APPLICATION DATA:
APPLICATION DATA:
APPLICATION - 435
FILING DATE: 07-JUN-1995
CLASSIFICATION UMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 10-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUN-1995
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUN-1995
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Best Local Similarity
APPLICATION NUMBER: US 07
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Newman, Roland APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BURNS,
STREET: 699 Princ
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FITLE OF INVENTION:
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TOPOLOGY: 1:-
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FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     ZIP: 22313-1404
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SOFTWARE: FastSE(
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COMPUTER: I
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             US 07/856,281
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for Windows Version 2.0
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FILING DATE:

25-JUL-1991

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US-08-476-349A-98
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                                                                                                                         FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/856,281
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Rab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCYDOKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rela
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: CHERRI
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Local Similarity 100.0%;
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Pred. No.
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US-08-958-201-10
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Best Local Similarity 100.0%;
                                                         Matches
                                                                     Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 120 amino acid
                                                                                                                                                                                                              APPLICATION NUMBER: US 60
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: ma
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                            IMMEDIATE SOURCE:
CLONE: 2Db
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                                                                                                                                                                       TOPOLOGY:
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CITY: Chicago
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TOPOLOGY: no
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                                                         Conservative
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Johnson, Kevin S
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00 Sears Tower, 233 South Wacker Drive
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                                                                   100.0%;
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                                                                   Score 97; DB 2;
Pred. No. 5.5e-08;
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Pred. No. 5.5e-08;
                                                         Mismatches
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RESULT 7 US-08-599-226-2

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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                             TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/08476349A Patent No. 5750105
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not rel MOLECULE TYPE: pept POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08, FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA: 97
APPLICATION NUMBER: US 07, FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07, A
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TRACET REAL ROLLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION:
TELECOMMUNICATION:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                               COUNTRY:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                             TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
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                                                                                                                                                                                    Alexandria
                                                                                                       22313-1404
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-22313-1404
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                                                                                                                                                                                                            699 Prince St.
                                                                                                                                  USA
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Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                       Newman, Roland A.
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O7-JUN-1995
ON: 435
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23-MAR-1992
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                                                                                                                                                                                                                                                                                                           Recombinant Antibodies for Human Therapy
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Pred. No. 5.7e-08;
0; Mismatches 0;
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Matches Query Match Best Local 9

l Similarity 20; Conservat

100.0%; silarity 100.0%; sometive 0;

TELEFAX: (617)2
INFORMATION FOR SEQ

SEQUENCE CHARACTERISTICS:

121 amino acids (617)227-5941 OR SEQ ID NO: 2:

FRAGMENT TYPE:

internal peptide TOPOLOGY: LENGTH:

amino acid )GY: linear

NAME: DeConti, Giulio A., Jr. REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617,227-7400

BBI-043

ATTORNEY/AGENT INFORMATION: NAME: DeConti, Giulio A.

CLASSIFICATION:

APPLICATION NUMBER: US/08/599,226 FILING DATE: 08-FEB-1996

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0

COUNTRY: USA ZIP: 02109-1875

Boston

Massachusetts

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

APPLICANT:

INFORMATION

Allen, <aymakcalan,

Hoogenboom, Hendricus

2ehra

Deborah J

Jochen G.

Application US/08599226

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: LAHIVE & COCKFIELD 60 State Street, suite 510

NUMBER OF SEQUENCES:

INVENTION: Andrew J.

Vaughan, Trist White, Michael Schoenhaut, David McGuinness, Brian T. Roberts, Andrew J. Labkovsky, Boris Mankovich, John A.

Tristan J.

US-08-478-039-99

Patent No. 5681722 GENERAL INFORMATION:

APPLICANT:

Newman, Roland A.

APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.

699 Prince St

Sequence 99, Application US/08478039 Patent No. 5681722

OPERATING SYSTEM:

Release #1.0, Version #1.30

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Best Local :
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INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
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APPLICATION NUMBER: US 07
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                     NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide POSITION IN GENOME: CHROMOSOME/SEGMENT: 18/2
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TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                     APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                               APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/379,072
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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FILING DATE: 10-JUL-1992
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                                                                                                       COUNTRY:
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                                                                                                                                   Palo Alto
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                                                                                                                                                                                                                                    Tang, Y. Tom
Yue, Henry
Au-Young, Janice
Corley, Neil C.
Guegler, Karl J.
Baughn, Mariah R.
                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                               Hillman, Jennifer L.
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FastSEQ for Windows Version
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RESULT 11
US-08-318-157B-30
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Best Local
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SEQUENCE CHARACTERISTICS:
                                                  ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION UNMBER: 28,665
REFERENCE/DOCKET NUMBER: 1873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HANSEN, Hans J.

APPLICANT: ARMOUR, Kathryn L.

TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: BMARN
CLONE: 1669829
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                            APPLICATION NUMBER: US/08/318,157B FILING DATE: 05-OCT-1994 CLASSIFICATION: 424
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REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                20007-5109
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                 USA
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                                   (202)672-5399
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                                                                                          18733/464
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Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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STRANDEDNESS:

amino acid

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RESULT 13
US-07-942-245-34
; Sequence 34, Application US/07942245
; Patent No. 5639641
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                                                                                                                                                                                                                                  ; TOPOLOGY: 11; MOLECULE TYPE: US-08-318-157B-31
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-30

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                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino
                                                                                                                                                           Matches
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 1873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HANSEN, APPLICANT: ARMOUR,
                                                                                                                                                         Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                              1 EVQLVESGGGLVQPGRSLRL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 95.0 les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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    Application US/08318157B
5874540

                                                                                                                                                                                                                                                                                           amino acid
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3000 K Street, N.W., Suite 500
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARMOUR,
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                                                                                                                                                                                                                                                  protein
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CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                       96.98;
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                                                                                                                                                                                                                                                                                                                                         31:
                                                                                                                                                   Score 94; DB 2;
Pred. No. 3.6e-08;
1; Mismatches (
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Pred. No. 3.6e-08;
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                                                                                                                                                      0,
                                                                                                                                                                                   Length 30;
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Best Local Similarity
Watches 19; Conserve
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US-08-652-558-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-07-942-245-34
         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERCE 6.1
CURRENT APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Applic Patent No. 5861155
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: PEDERS
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION UNBER: US/07/942,245
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                        STREET: 75 ST
CITY: BOSTON
STATE: MASSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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   APPLICATION NUMBER:
                                                                                                                                                                          COUNTRY:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                           02109
                                                                                                                                                                                                                                                                                                                                                               Application US/08652558
                                                                                                                                                                                       MASSACHUSETTS
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                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                 AUGUSTINE YEE-THARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.9%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthony R.
Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
                                                                                                                                                                                                                                                                                               HUMANIZED ANTIBODIES AND USES
PCT/IB94/00387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephen M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 94; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                      1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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FILING DATE: NOVEMBER 21 ATTORNEY/AGENT INFORMATION: NAME: YANKWICH, LEON R.

NOVEMBER 21, 1994

REGISTRATION NUMBER:

30,237

95,497-L

0,:

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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-91100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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US-08-652-558-44
                                                                                                                                                                  ; MOLECULE TYPE: US-08-652-558-44
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION OBTA:
APPLICATION OB
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEPAY. 617-745-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 44, Application US/08652558 tent No. 5861155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: BANKER 6 WITCOFF
ADDRESSEE: BANKER 6 WITCOFF
STREET: 75 STATE STREET, 23F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 75 ST
CITY: BOSTON
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                           SS: single
linear
                                                                                                                                                                                                  protein
    96.98;
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    Score 94; DB 2;
Pred. No. 1.5e-07;
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Pred. No. 1.5e-07;
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                                            Length 117;
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         δõ
                   Matches
19; Conservative
                  1;
                   Mismatches
                   0;
                   Indels
                   0;
                  Gaps
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Search completed: June 13, 2001, 14:27:09 Job time: 630 sec

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Minimum DB :
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                             score greater than and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
100.0
57.0
57.0
57.0
54.4
54.4
54.4
54.4
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                                                                                                                                                                                                                                                                                                                                        is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                             Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                               June 13, 2001, 14:25:51; Search time 150.28 Seconds (without alignments) 5.325 Million cell updates/sec
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/SIDS6/qcqdata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390729 seqs, 57163235 residues
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Gapop 10.0 , Gapext 0.5
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:/SIDS6/gcgdata/geneseq/geneseqp/An198.DaT:*
:/SIDS6/gcgdata/geneseq/geneseqp/An198.DaT:*
:/SIDS6/gcgdata/geneseq/geneseqp/An198.DaT:*
:/SIDS6/gcgdata/geneseq/geneseqp/An198.DaT:*
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/SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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                                                                                               G39903
G39902
G24558
                                                                                                                                                          R20006
Y79110
G39904
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      Zonula occludens t
Peptide antagonist
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human zona pelluci
Human zona pelluci
Human zona pelluci
                                                                                                                                                                                                                                         Description
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	R55194	15	713	46.8	37	45
Peptide antagonist	Y79114	21	8	46.8	37	44
ptus grandi	в25110	21	903	48.1	38	43
Human secreted pro	B40159	21	36	48.1	38	42
	Y79122	21	8	48.1	38	41
de an	Y79109	21	8	48.1	38	40
ZP2 prote	R06998	11		•	40	39
zona	Y52977	21	716		41	38
	Y52173	21	716		41	3 <b>7</b>
	Y52682	21	716	51.9	41	36
zona	Y82208	21	716	•	41	35 5
ZPA p	W81810	20	716		41	34
zona	Y42473	20	716	•	41	ω ω
zona	R60532	15	716	•	41	32
zona	R55200	15	716	•	41	31
zona	Y52975	21	715		41	30
zona pe	Y52171	21	715		41	29
oocyt	Y52680	21	715		41	28
zona	Y82206	21	715		41	27
ZPA p	W81808	20	715	•	41	26
zona	Y42471	20	715	٠	41	25
zona	R55198	15	715		41	24
Canine zona pelluc	R60101	15	713	51.9	41	23
Chlamydia pneumoni	Y34767	20	200		41	22
Cyclic peptide of	W52566	19	13		41	21
Peptide antagonist	Y79106	21	æ		42	20
Nematode extracted	Y30410	20	181	٠	N	19
· AcaNAP47. Ancylos	R91712	17	181		42.5	18
A. caninum nematod	B15322	21	162		N	17
nematode	Y30437	20	162		N	16
e nematode e	w	20	84	٠	N	15
zona pelluc	5298	21	745		43	14
zona pe	Y52180	21	745	54.4	43	13
Human oocyte zona	Y52689	21	745	54.4	43	12

## ALIGNMENTS

RESULT

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DE COS CONTRACTOR OF CONTRACTO
                                                                                                                                     New Vibrio cholerae strains - comprise restriction endonuclease fragment encoding toxin, used as vaccines against cholera
                                                                                                                                                                                                                                                                                                      WPI; 1992-007465/01.
N-PSDB; Q20185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaper JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZOT; cholera; vaccine; enterotoxin; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zonula occludens toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R20006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R20006 standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0533315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-US03812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fasano A;
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Disclosure; Fig 18; 83pp; English

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Best Local
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This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (20T) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for
                                                                                                                                                                                                                                                                                                 New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigeilosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zonulin; antagonist; zonula occiudens coxin receptor, blood-brain barrier; antiinflammatory; cerebaroprotective; dermatological; antiuncer; antiviral; neuroprotective; dermatological; antiuncer; antifal
                                                                                                                                                                                                                                                                  Claim 1; Page 42; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-205565/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid sequence is that of the zonula occludens toxin (207). It may be responsible for diarrhoea in some strains of cholera and the ZOT gene or fragments of it are deleted from strains of vibrio cholerae (V.c.) to be used as vaccines. These V.c. strains have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodn. of vaccines against cholera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic;
hypotensive; immunosuppressive; antiparasitic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide antagonist of zonulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y79110 standard; Peptide;
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| 288 fcigrlcvqdgfvt 301
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Pred. No.
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RESULT
G39904
ID G3
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Best Local Similarity
Matches 8; Conser
            28-APR 1999;
30-APR 1999;
30-APR 1999;
04-MAY 1999;
05-MAY 1999;
06-MAY 1999;
06-MAY 1999;
07-MAY 1999;
11-MAY 1999;
11-MAY 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangiectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                                                      23-APR-1999,
23-APR-1999,
                                                                                                                                                                                                   08-APR-1999;
                                                                                                                                                                                                                06-APR-1999
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01-APR-1999;
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25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 49440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G39904 standard; Protein; 751 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. systemic lupus milk.
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99US-0131449
99US-0132048
99US-0132487
99US-0132484
99US-0132485
99US-0132486
99US-0132486
99US-0132863
99US-0134256
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99US-0134258
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99US-0127462.
99US-0128234.
99US-0128714.
99US-0128714.
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99US-0130449.
99US-0130510.
99US-0130891.
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99US-0123548
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promoter;
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16-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 22-AUG-1999; 23-AUG-1999; 24-AUG-1999; 27-AUG-1999; 28-EP-1999; 29-SEP-1999; 21-AUG-1999; 21-AUG-1999; 21-AUG-1999; 22-AUG-1999; 23-SEP-1999; 24-SEP-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 28-EP-1999; 29-SEP-1999; 21-AUG-1999; 21-AUG-	27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 07-AUG-1999; 08-AUG-1999; 09-AUG-1999; 10-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999;
16-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG	27-JUL-1999 99US 27-JUL-1999 99US 27-JUL-1999 99US 28-JUL-1999 99US 28-JUL-1999 99US 02-AUG-1999 99US 02-AUG-1999 99US 03-AUG-1999 99US 04-AUG-1999 99US 05-AUG-1999 99US 06-AUG-1999 99US 07-AUG-1999 99US 08-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US
16-AUG-1999 17-AUG-1999 29US-011 20-AUG-1999 29US-012 20-AUG-1999 29US-012 20-AUG-1999 29US-012 20-AUG-1999 29US-012 20-AUG-1999 29US-012 21-AUG-1999 29US-013 21-AUG-1999 29US-0	27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 28-JUL-1999; 99US-014 02-AUG-1999; 99US-014 02-AUG-1999; 99US-014 03-AUG-1999; 99US-014 04-AUG-1999; 99US-014 05-AUG-1999; 99US-014 05-AUG-1999; 99US-014 06-AUG-1999; 99US-014 06-AUG-1999; 99US-014 07-AUG-1999; 99US-014 08-AUG-1999; 99US-014 09-AUG-1999; 99US-014 09-AUG-1999; 99US-014 11-AUG-1999; 99US-014
16-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG	27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 28-JUL-1999; 99US-014 02-AUG-1999; 99US-014 02-AUG-1999; 99US-014 03-AUG-1999; 99US-014 04-AUG-1999; 99US-014 05-AUG-1999; 99US-014 05-AUG-1999; 99US-014 06-AUG-1999; 99US-014 06-AUG-1999; 99US-014 07-AUG-1999; 99US-014 08-AUG-1999; 99US-014 09-AUG-1999; 99US-014 09-AUG-1999; 99US-014 11-AUG-1999; 99US-014
16-AUG-1999 17-AUG-1999 99US-011 18-AUG-1999 99US-012 20-AUG-1999 99US-012 20-AUG-1999 99US-012 20-AUG-1999 99US-012 21-AUG-1999 99US-012 22-AUG-1999 99US-013 22-AUG-1999 99US-013 22-AUG-1999 99US-013 22-AUG-1999 99US-013 22-AUG-1999 99US-013 23-AUG-1999 99US-013 23-AUG-1999 99US-013 24-SEP-1999 99US-013 25-SEP-1999 99US-013 26-SEP-1999 99US-013 27-AUG-1999 99US-013 28-SEP-1999 99US-013 29-SEP-1999 99US-013 21-SEP-1999 99US-013 22-SEP-1999 99US-013 23-SEP-1999 99US-013 24-SEP-1999 99US-013 25-SEP-1999 99US-013 26-CCT-1999 99US-013 26-CCT-1999 99US-013 27-CCT-1999 99US-013 28-CCT-1999 99US-013 29-CCT-1999 99US-013 21-CCT-1999 99US-013 21-CCT-1999 99US-013 21-CCT-1999 99US-013 21-CCT-1999 99US-013 22-CCT-1999 99US-013	27-JUL-1999; 99US-012 27-JUL-1999; 99US-012 27-JUL-1999; 99US-013 28-JUL-1999; 99US-013 02-AUG-1999; 99US-013 02-AUG-1999; 99US-013 03-AUG-1999; 99US-013 04-AUG-1999; 99US-013 05-AUG-1999; 99US-013 05-AUG-1999; 99US-013 06-AUG-1999; 99US-013 06-AUG-1999; 99US-013 06-AUG-1999; 99US-013 07-AUG-1999; 99US-013

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RESULT
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Best Local S
Matches
        23-APR-1999;
28-APR-1999;
30-APR-1999;
04-APR-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
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09-WAR-1999

23-WAR-1999

25-WAR-1999

29-WAR-1999

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08-APR-1999
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05-MAR-1999;
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4 yclgrmcvpepf 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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       990S-0121825

990S-0123580

990S-0125788

990S-0126785

990S-0127462

990S-012785

990S-0129845

990S-013047

990S-013049

990S-013049

990S-0132484

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990S-0132484

990S-0132485

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990S-0132486

990S-0134786

990S-0134768

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990S-0134768

990S-0134741

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990S-0161360.
990S-0161359.
990S-0161361.
990S-0161361.
990S-0161992.
990S-0161992.
990S-0161993.
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Pred. No. 22;
4; Mismatches
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  25-MAY-1999
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28-MAY-1999
01-JUN-1999
04-JUN-1999
07-JUN-1999
10-JUN-1999
11-JUN-1999
11-JUN
99US-0136021

99US-0136782

99US-0137722

99US-0137722

99US-0137723

99US-0137528

99US-0138647

99US-0139453

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99US-0139450

99US-014905

99US-014905

99US-0146085

99US-0144331

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99US-0145086

99US-0145246

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25-MAR-1999
25-MAR-1999
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16-APR-1999
23-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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Similarity 50.0%;
6; Conservative
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99US-0121825

99US-0125788

99US-0126786

99US-0126786

99US-0126786

99US-0128714

99US-0128714

99US-013049

99US-013049

99US-013049

99US-013048

99US-013149

99US-0132486

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99US-013471

99US-013502

99US-013502
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99US-0162142.
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promoter;
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.03-AUG-1999
.04-AUG-1999
.05-AUG-1999
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.06-AUG-1999
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.07-AUG-1999
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.09-AUG-1999
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09-AUG-1999
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10-JUN 1999
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9908-013804
9908-013804
9908-0138119
9908-0139452
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9908-0145086

Query Match Best Local S Matches 6 6; Conserv Conservative 4: Score 45; DB Pred. No. 25; 4; Mismatches 2; Indels 0,

57.0%;

Gaps

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G24558;
ID4588;
ID4588;
ID4588;
XX

XX

XX

AC G24558;
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AC G24558;
XX

DT 17-OCT-
DX

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XW termina
XW termina
XW termina
XW termina
XW EP10334
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EP1034
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EP10334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis
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0 yclgrmcvpepf 181
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990S-012548
990S-0126785
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expression control; promoter;
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    18-JUN 1999
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9905-01477493.
9905-01477493.
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RESULT
R74094
                    В
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                                                                Query Match
Best Local S
Matches 7
                    208
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                    fcigrlc 214
                                         7; Conserv
                                         54.4%; So ilarity 100.0%; I Conservative 0;
                                                                                                                                                     9908-0155486

9908-0156596

9908-0156596

9908-015717

9908-0157865

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9908-0158232

9908-0158232

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99US-0149722
99US-0149723
99US-0149923
99US-0149930
99US-0150866
99US-0150884
99US-0151065
                                               Score 43;
Pred. No.
                                         Mismatches
                                              DB
18;
                                                    21;
                                         0
                                                   Length 284;
                                         Indels
                                         0
                                        Gaps
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RESULT
R55206
ID R5
XX
AC R5
Query Match
Best Local S
Matches 7
         06-NOV-1993;
                                   26-MAY-1994.
                                                                                                                                      Homo sapiens
                                                                                                                                                                 Human; zona pellucida; ZPA; immunocontraception.
                                                                                                                                                                                           Human zona pellucida ZPA protein.
                                                                                                                                                                                                                     01-FEB-1995
                                                                                                                                                                                                                                               R55206;
                                                                                                                                                                                                                                                                      R55206 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The human zona pellucida-2 (HZP-2) protein may be used as a vaccine antigen. It can be artificially synthesised using recombinant techniques. Partial sequences of the HZP-2 gene were subcloned, the sequences and primers used in cloning and subcloning are given in 092255-69.
                                                            WO9411019-A.
                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 8-11; 11pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DNA coding human zona pellucida-2 protein - used as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-182067/24.
N-PSDB; Q92254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP07099974-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zona pellucida; HZP-2; protein; vaccine; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zona pellucida-2 (HZP-2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R74094 standard; Protein; 742 AA.
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369 gelctqdgfm 378
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity 70.07; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         742 AA;
                                                                                                                                                                                                                    (first entry)
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         93WO-US10851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0249404
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                                                                                  Location/Qualifiers
1..745
/label= human_ZPA
                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                    54.4%;
70.0%;
                                                                                                                                                                                                                                                                        745 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japanese
                                                                                                                                                                                                                                                                                                                                                                                        ; Score 43; DB;
; Pred. No. 46;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                               Length 742;
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Best Local S
Matches 7
                                                                                                       09-NOV-1993;
09-NOV-1992;
29-JAN-1993;
                                                                                                                                                                                                                            Contraceptive; porcine; pig; zona dog; rabbit; feline; cat; bovine; zPB; zPC; infertility; veterinary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9-23kb inserts of DNA from placenta tissue of a male caucasian cloned into the Lambda Fix (RTM)II vector was screened with probes encoding porcine ZPA and ZPB proteins. Positive clones were analysed further by Southern hybridisation using the porcine probes and restriction analysis. Clones encoding human ZPA and ZPB proteins were identified (see 055616 and 055617 respectively).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of zona pellucida proteins and reproducible transient infertility female mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1992;
29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A commercially available human genomic DNA library consisting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 40; Page 126-128; 154pp;
                                     WPI; 1999-633318/54
N-PSDB; Z22737.
                                                                                                                                                07-JUN-1995;
                                                                                                                                                                    09-NOV-1999
                                                                                                                                                                                       US5981228-A
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                   Human zona pellucida ZPA protein
                                                                                                                                                                                                                                                                                                            Y42480
                                                                                                                                                                                                                                                                                                                              Y42480 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q65616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-183156/22.
         infertility
                 Mammalian zona pellucida
                                                                   Podolski
                                                                                     (ZONA-) ZONAGEN
                                                                                                                                                                                                                                                                                        15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                 4 GRLCVQDGFV 13
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gelctqdgfm 378
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 70.07; Conservative
                                                                  JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 AA;
                                                                                                                                                                                                                                                                                       (first entry)
                                                                  HSu KT,
                                                                                                       93US-0149223.
92US-0973341.
93US-0012990.
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93US-0012990.
                                                                                                                                                95US-0484596
                                                                                     INC.
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                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                             54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Podolski JS;
                                                                  Harris
                 proteins
                                                                                                                                                                                                                                                                                                                              745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB Pred. No. 47; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                 used
                                                                                                                                                                                                                                      pellucida; mammal;
cow; human; cynomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies - or permanent
                                                                                                                                                                                                                                                                                                                                                                                                                            DB
47;
                 to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                      cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for inducing sterility in
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 745;
                 transient
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                      lapine; canine;
lgus monkey; ZPA;
                 or
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                 permanent
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                   09-NOV-1993;
09-NOV-1992;
29-JAN-1993;
07-JUN-1995;
                   This sequence represents a human ZPA protein isolated from zona pellucida. This protein can be used in a method for specifically inducing transient infertility or permanent sterility in a host animal by selective vaccination with specific zona pellucida proteins or immunocontraceptively active fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human zona pellucida ZPA protein. The invention relates to the isolation of novel nucleotide sequences ence zona pellucida proteins from mammalian, especially porcine, lapine, canine, feline, bovine, human or cynomolgus monkey sources. The zona pellucida proteins (ZPA, ZPB, and ZPC) are used in the induction of transient or permanent infertility. At present the method is used in veterinary applications to induce transient or permanent infertility
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ZPA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W81817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W81817 standard;
                                                                                                                         Isolated zona pellucida DNA from different mammals - products which can be used for vaccination to induce infertility or permanent sterility in female mammals
                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                   US5837497-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                Example 11; Column 133-138; 84pp; English.
                                                                                                                                                                            WPI; 1999-023447/02.
N-PSDB; V64814.
                                                                                                                                                                                                                                                                                                                                                           17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1999
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                                                                                                                                                                                                                    Harris
                                                                                                                                                                                                                                          (ZONA-) ZONAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Column 127-132; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GRLCVQDGFV 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                zona
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|gelctqdgfm 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 70.7
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                pellucida;
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745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lapine,
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92US-0973341.
93US-0012990.
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                                                                                                                                                                                                                                                                                                                                  95US-0484993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           canine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                infertility; sterility; immunocontraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB Pred. No. 47; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bovine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 745
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                                                                                                                                        transient
                                                                                                                                                   used to develop
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Query Match
Best Local Similarity

54.48; 70.08;

Score Pred.

N 43.

DB 20; 47;

Length .745;

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                                                                                                                                                   Query Match
Best Local :
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                      immunologically active fragment selected from feline, bovine, cynomologous monkey or human ZPB polypeptides; (2) an isolated, purified recombinant feline, bovine, cynomologous monkey or human ZPB polypeptide or immunologically active fragment; and (3) a fusion protein comprising a ZPB polypeptide which is conjugated with a compound selected from keyhole limpet haemocyanin, muramyl dipeptide, histidine-tag, beta-gal, or palmitic acid where the fusion protein remains effective to stimulate production of antibodies that recognise a ZPB polypeptide. The method is useful for providing transient or permanent infertility or sterility in humans and animals. The present sequence represents human ZPA, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administration of homologous and/or heterologous mammalian species zona pellucida (ZP) proteins or immunocontraceptively active fragments. Also described are: (1) a method for inducing transient infertility in mammal by administering directly an antibody directed to a ZPB or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for inducing reproducible transient infertility in a female mammal, including humans, by selvents to the contract of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing reproducible transient or permanent infertility in a mammal comprises administration of homologous and/or heterologous mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1992;
29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zona pellucida; ZPA; ZPB; ZPC; vaccine; immunocontraceptive; c
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                   used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Column 135-138; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Z95674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-269144/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zona pellucida ZPA SEQ ID NO:43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y82215 standard; Protein; 745 AA
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      369
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369 gelctqdgfm 378
                                                                                                                    Local Similarity
nes 7; Conserv
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                                                           4 GRLCVQDGFV 13
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gelctqdgfm 378
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                                                                                                                                                                                                                                                                           745 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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93US-0012990.
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                                                                                                                                                   54.48;
70.08;
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                                                                                                                                                                                                                                                                                                                                   of the present invention.
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                                                                                                                                                   Score 43; DB Pred. No. 47;
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contraceptive; immunostimulatory.
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                Length 745;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 12
Y52689
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Best Local Similarity
""" 7; Conserve
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Y52180
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09-NOV-1992;
29-JAN-1993;
                                                                                                                                                                                                                                                                                  polynucleotides encoding zona pellucida proteins from other mammalian species. Administration of zona pellucida proteins to a host animal results in a specific immunocontraceptive effect. Administration of purified ZPA and/or ZPB induces transient infertility in females. Fertility can be maintained in an on or off condition in a controllable/predictable fashion. Administration of ZPC induces permanent sterility. Use of a purified zona pellucida protein rather than a complex mixture of zona pellucida proteins reduces the potential for unwanted side-effects which may be harmful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zona pellucida; ZPA; ZPB; ZPC; purified; mammalian; glycoprotein; target; immunocontraception; vaccine; antibody; transient; infert controllable; predictable; permanent; sterility; side effect.
            Y52180
                                                                                                                                                                                                                                                                                                                                                                                                                          encoding these proteins can be used for recombinant protein production and as probes in hybridisation methods for the isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      oocyte, formed of glycoproteins secreted by ovarian cells. The invention relates to zona pellucida proteins ZPA, ZPB and ZPC, which are useful as targets for immunocontraceptive vaccines. Polynucleotides
                                         Y52180 standard; Protein; 745
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a mammalian zona pellucida protein, zPA The zona pellucida is a complex matrix surrounding the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Columns 133-136; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated DNA encoding mammalian zona pellucida proteins useful for inducing transient sterility - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y52689 standard; Protein; 745 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Podolski JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZONA-) ZONAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000
                                                                                                                   369 gelctqdgfm
                                                                                                                                                4 GRLCVQDGFV 13
                                                                                                                                                                                                                                                           745
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zona pellucida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hsu KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0149223.
92US-0973341.
93US-0012990.
                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0458731
                                                                                                                                                                                               54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                            Score 43;
                                                                                                                                                                                               Pred. No.
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZPA.
                                                                                                                                                                                                            DB
                                                                                                                                                                                                            21;
                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                            Length 745;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infertility;
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RESULT
Y52984
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     X X X E X D X A X B
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biologically active fragments also porcine and cynomologus monkey ZPA. The zona pellucida is a complex matrix surrounding the mammalian occyte, formed of glycoproteins secreted by ovarian cells. The previously mentioned ZPA proteins can be used to produce a fusion protein to stimulate production of antibodies in a mammal that recognize a ZPA polyeptide of the mammal. The ZPA polypeptides are useful as vaccines for selectively effecting transient infertility in mammals. ZP has an important role in maintaining the occyte and in occyte-sperm interactions and so is a target for a contraceptive agent which interferes with the fertilization process. Providing a specific polypeptide reduces the need for a complex mixture of many ZP proteins which may create unwanted and harmful side effects. The duration of transient fertility is controllable and can be maintained in a controllable and/or predictable fashion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1993;
09-NOV-1992;
29-JAN-1993;
Zona pellucida; ZPA; immunocontraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the human zona pellucida The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated and purified mammalian zona pellucida proteins useful methods of immunocontraception - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5989550-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-2000 (first entry)
                                                                       Human zona pellucida
                                                                                                                         14-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-022762/02.
N-PSDB; Z37821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human zona pellucida protein
                                                                                                                                                                                                                       Y52984 standard; Protein; 745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the human zona pellucida protein B (ZPB) amino acid sequence. The invention relates to isolated and purified zona pellucida proteins from mammals, specifically canine, feline and bovine ZPA or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Column 133-136; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Podolski JS, Hsu KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZONA-) ZONAGEN INC.
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Lmmunocontraceptive.
                                                                                                                                                                                                                                                                                                                                               369 gelctqdgfm 378
                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                           4 GRLCVQDGFV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 AA;
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0149223.
92US-0973341.
93US-0012990.
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ZPB; ZPC; infertility; sterility; vaccine;
contraception; immunisation.
                                                                       ZPA protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB
Pred. No. 47;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZPB; ZPC; oocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pocyte; ovarian cell; antibody;
fertilization; fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 745;
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Best Local S
Matches 7
19-APR-1996;
18-OCT-1994;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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09-NOV-1993;
09-NOV-1992;
29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically ZPC proteins. Also described are fusion proteins of ZPC with any of keyhole limpet haemocyanin, muramyl dipeptide, histidine tag, beta-galactosidase or palmitic acid, capable of stimulating mammalian antibodies that recognise mammalian ZPC. Recombinant ZPC proteins are used to immunise animals to induce transient infertility or permanent female sterility, in humans or other mammalis. Z33243 to Z33254, Z33270 to Z33274 and Z33285 encode mammalian ZP proteins given in Y52971 to Y52988 from the present invention. Z33255 to Z33269 and Z33275 to Z33284 represent oligonucleotides used in the exemplification of the present
                                                                                                                    US5955294-A.
                                                                                                                                                                              Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.
                                                                                                                                                                                                                          Mature nematode extracted anticoagulant protein AcaNAP47d1.
                                                                                                                                                                                                                                                                                                                    Y30424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Column 133-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant mammalian zona pellucida C proteins, female sterility .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5976545-A
                                                          19-APR-1996;
                                                                                        21-SEP-1999
                                                                                                                                                  Ancylostoma
                                                                                                                                                                                                                                                           15-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZONA-) ZONAGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                           4 GRLCVQDGFV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes recombinant zona pellucida (2P) proteins, pifically ZPC proteins. Also described are fusion proteins of ZPC with
                                                                                                                                                                                                                                                                                                                                                                                             gelctqdgfm 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-037080/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsu KT,
96US-0634641.
94US-0326110.
95US-0461965.
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92US-0973341.
93US-0012990.
                                                          96US-0634641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0484158
                                                                                                                                                                                                                                                                                                                     Protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87pp; English

    Mismatches

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Pred. No.
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                                                                                                                                                                                                                           The present sequence represents a nematode extracted anticoagulant CC proteal (NAP). The protein has activity as an anticoagulant and/or serine protein (NAP). The protein contains at least one NAP domain which CC protease inhibitor. The protein contains at least one NAP domain which CC has selective inhibitory activity for factor VIIa/TF. The specification CC describes a method for screening an isolated protein at least one domain CC for factor VIIa/TF selective inhibitory activity. The method comprises CC determining the time to clotting effected by a concentration of the CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo CC activated partial thromboplastin time (aPTT) assay; calculating CC prolongation of clotting effected by the isolated protein in each of CC the PT and aPTT parolongation of clotting is calculated as fold CC elevation of clotting time relative to a baseline clotting value, where CC alculating of clotting time is deemed a two-fold elevation; and CC calculating of clotting time is deemed a two-fold elevation; and CC useful to a protein has factor VIIa/TF inhibitory activity. The method is constituted if a protein has factor VIIa/TF inhibitory inhibitory
                                                                           Query Match 53.6
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
17-OCT-1995;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                    activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-539569/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bergum PW, Gansemans YGJ,
Lauwereys MJ, Messens JHL,
Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Columns 135-138; 197pp; English.
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2 CIGRLCVQD-GF 12
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46 cigrvcvcdegf 57
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95US-0486397.
95US-0486399.
95WO-US13231.
                                                                                                53.8%;
75.0%;
                                                                           Score 42.5; DB Pred. No. 6.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jespers LS, Laroche YR;
Moyle M, Stanssens PEH;
                                                                                                                  DB 20;
                                                                                                              Length 84;
                                                                             Indels
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Search completed: June 13, 2001, 14:25:51 Job time: 670 sec

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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40.5
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79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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pir2:*
pir3:*
pir4:*
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10.937 Million cell updates/sec
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VGIH59
VGIHJ2
JQ1534
D82364
T39757
S41400
S69194
S74601
S74601
                                                                                                                           $70397
$70398
T46027
T24018
T01352
T05868
A34782
                                                                                                                                                                                              B82197
A43864
A45984
A48833
T16805
G72580
C72112
B64041
         T34189
T26723
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N4-(beta-N-acetylg
hypothetical prote
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        hypothetical
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C; Genetics: A; Gene: VC1458 A; Map position:

position: 1

A;Accession: B82197 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-399 <hei> A;Cross-references: GB;AE004224; A;Experimental source: serogroup C;Genetics:</hei>	l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the chc A; Reference number: A82035; MUID:20406833	C;Date: 18-Aug-2000 #sequence_revision 20-Aug- C;Accession: B82197 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.;	RESULT 1 B82197 zona occludens toxin VC1458 C:Species: Vibrio cholerae		44 37 45 37	ω	41 37 42 37					35 38					
Hainary e: DNA 399 <hei> nces: GB:AE004224;</hei>	nos, J.J 7-483, 20 equence o	-2000 #se 32197 J.F.; Eis Ermolaeva	toxin VC		46.8		46.8	•		A 60 00 00		48.1	48.1	48.1	48.1	48.1	
AE0042: serogro	.; Vent 00 f both 035; M	quence en, J./ , M.D.	ω		613 713	524	432 468	386	309	161	331	2946	508	869	497	493	
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GB:AE00385; O1; strain	J.C.; Frase comosomes of 20406833	g-2000 #sequence_revision 20-Aug-2000 #- B82197 J.F.; Eisen, J.A.; Nelson, W.C.; Claytu Ermolaeva, M.D.; Vamathevan, J.; Bass,	[imported] - Vil	ALIGNMENTS	T42671 S70434	JN0606	G64133 D70557	A82284	B82460	S61389	E70367	T15840	S64238	JX0202	S66834	E71008	
GB:AE003852; NID:99655952; PIDN:AAF94615.1; GSPDB:GN Ol; strain N16961; biotype El Tor		#sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. aeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers	Vibrio cholerae (group O1 strain N16961)	NTS	hypothetical prote zona pellucida gly	ATP-stimulated glu	adenylosuccinate s probable lat prote	conserved hypothet	hypothetical prote	small basic protei	phosphoribosylform	nypornerical prote	kinesin-related pr	long-chain-fatty-a	probable membrane	hypothetical prote	

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Zonula occludens toxin - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A43864
R;Baudry, B.; Fasano, A.; Ketley, J.; Kaper, J.B.
Infect. Immun. 60, 428-434, 1992
A;Title: Cloning of a gene (zot) encoding a new toxin produced b
A;Reference number: A43864, MUID:92112300
A;Accession: A43864
A;Status: preliminary
A;Status: preliminary
                                                            A;Cross-references: GB:M83563; NID:g155314; PIDN:AAA27582.1; PID:g155315 A;Note: sequence extracted from NCBI backbone (NCBIN:77488, NCBIP:77491)
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                                                                                             A; Molecule type: DNA
A; Residues: 1-399 <BAU>
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Query Match
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Pred. No.
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79;
No.
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ches 0;
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C;Superfamily: sperm-binding glycoprotein ZP2; Z
C;Keywords: glycoprotein; oocyte; transmembrane
F;371-631/Domain: ZP domain homology <ZPH>
                       RESULT
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A; Residues: 1-745 <LIA>
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Dev. Biol. 156, 399-408, 1993
A:Tille: Conservation of mammalian secondary sperm receptor A:Reference number: A48833; MUID:93215931
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A; Residues: 1-676 < LESS
A; Cross-references: GB:L12167
C; Superfamily: sperm-binding glycoprotein ZP2;
C; Keywords: glycoprotein; oocyte; transmembrand
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R;Lee, V.H.; Schwoebel, E.; Prasad, S.; Cheung, P.; Timmons, T.M.; Cook, R.; Dunbar, J. Biol. Chem. 268, 12412-12417, 1993
A;Title: Identification and structural characterization of the 75-kDa rabbit zona pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: ZP2
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N;Alternate names: 75K zona pellucida glycoprotein;
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A;Accession: A45984
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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70.0%;
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A; ACCESSION.
A; Residues: 1-195 < ARN\
A; Cross-references: GB: AE001603; GB: ACCESSION A; Cross-references: GB: AE001603; GB: ACCES A; Cross-references: GB: AE001603; GB: AE001603;
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A; Title: Comparative genomes of Clamydia pneumoniae A; Reference number: A72000; MUID:99206606
A; Accession: C72112
                                                             R; Kalman, S.; Mitchell, W.; Nature Genet. 21, 385-389,
                                                                                                   hypothetical protein CP0606 [imported] - Chlamydophila pneumoniae (strains CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: C72112; D81559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           awa, H.; Takamiya, M.; Masuda, DNA Res. 6, 83-101, 199
A;Title: Complete genome sequer A;Reference number: A72450; MUJ
A;Accession: G72580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein APE1926 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: G72580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DNAA; Residues: 1-256 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid T05A7 A; Reference number: Z18580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T05A7.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T16805
                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Kawarabayasi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Ya. M.; Masuda, S.; Funahashi, T.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDBJ:AP000062; NID:g5105244; PIDN:BAA80932.1; PID:d1044718; PID:g
ce: strain K1
                                                                              W.; Marathe, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of an aerobic hyper-thermophilic Crenarchaeon,
50; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                       51.9%;
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Pred. No.
2; Mismatc
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Pred. No.
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7.4;
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                                                                              Fan, J.; Olinger, L.;
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GB:AE001363; NID:g4376422; PIDN:AAD18318.1;

PID:9437

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A;Gene:

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from

A.G.

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phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) Cj1529c [imported] -
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: G81299
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein HI1730 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000.
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
                                                                  A;Cross-references: GB:AL139078; A;Experimental source: serotype (
                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <PAR>
                                                                                                                                                                    A;Title: The genome sequence of the food-borne pathogen A;Reference number: A81250; MUID:20150912 A;Accession: G81299
                                                                                                                                                                                                                             C.W.; Quail, M.; Rajandream, M.A.;
Nature 403, 665-668, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-195 <REA>
A;Cross-references: GB:AE002218; GB:AE002161;
A;Experimental source: strain AR39, HL cells
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A;Accession: B64041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; A;Title: Whole-genome random sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: B64041
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Best Local S
Matches 8
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                             Cj1528; Cj1529c
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7; Conserv
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8; Conser
    phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglyci
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                                                                  GB:AL111168; NID:g6968723; PIDN:CAB73945.1; O2, strain NCTC 11168
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Pred. No.
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Pred. No.
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14;
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                                                                                                                                                                                                                                             ; Churcher,
VanVliet, A
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hypothetical protein T10K17.260 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
                                                                RESULT
T46027
                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-716 < HAR>
A; Residues: 1-716 < HAR>
A; Cross-references: EMBL.U05776; NID:9458268; PIDN:AAA74388.1; PID:9458269
C; Superfamily: sperm-binding glycoprotein zP2; ZP domain homology
F; 370-630/Domain: ZP domain homology <ZPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Harris, J.D.; Hibler, D.W.; Fontenot, G.K.; DNA Seq. 4, 361-393, 1994
A;Title: Cloning and characterization of zona A;Reference number: S70396; MUID:95143578
A;Accession: S70398
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997
C;Accession: S70398
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DNA Seq. 4, 361-393, 1994
A;Title: Cloning and characterization of:
A;Reference number: $70396; MUID:95143578
A;Accession: $73397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zona pellucida glycoprotein A - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Oct-1996 #sequence_revision
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A; Residues: 1-715 <HAR>
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les 6; Conser
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Pred. No.
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C;Accession: T46027
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23019
A;Accession: T46027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 3
A; Introns: 31/3; 1:
A; Note: T10K17.260
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A;Residues: 1-1209 <BEN>
A;Cross-references: EMBL:AL132977
A;Experimental source: cultivar Columbia; BAC clone T10K17
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Arabidopsis thaliana hypothetical protein T10K17.260
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A; Introns: 61/1; 107/3; 317/3; 351/3
C; Superfamily: alpha-galactosidase
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submitted to the EMBL Data Library, July 1996
A; Reference number: Z19830
A; Accession: T24018
A; Accession: T24018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein R07B7.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T24018
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                                         A; Molecule type: DNA
A; Residues: 1-475 < RYA>
                                                                                                     A; Description: The sequence of A; Reference number: Z14297 A; Accession: T01352
                                                                                                                                                               C;Accession: T01352
R;Ryan, E.; Edwards, J.; Pape, K.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                          hypothetical protein F6N15.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:R07B7.11
A; Experimental
                                                                             A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-451 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:275955; PIDN:CAB00120.1; GSPDB:GN00023; CESP:R07B7.11
Experimental source: clone R07B7
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Cross-references: EMBL:AF069299; NID:g3193311; PID:g3193319; Experimental source: cultivar Columbia
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Pred. No. 61;
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A;Cross references: EMBL:AL035602
A;Experimental source: cultivar Columbia; BAC clone T29A15
C;Genetics:
A;Map position: 4
A;Introns: 76/3; 108/3; 146/2; 211/3; 285/2; 319/1; 354/1; 394/2; 43
A;Note: T29A15.120
C;Superfamily: Arabidopsis thaliana hypothetical protein T29A15.120
                                                                                                                                                                                                                                                                                                                               R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, submitted to the Protein Sequence Database, March 1999 A;Reference number: 215455 A;Accession: T05868 A;Molecule type: DNA A;Residues: 1-631 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T29A15.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 24-Nov-1999 C;Accession: T05868
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A; Note: F6N15.2
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DPOL_ROWH
VGL2_CVMAH
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RSPC_FLANE
C4A2_DROME
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p48829 oryctola
Q05996 homo sap
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4 schizosacch
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8 drosophila
1 caenorhabdi
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1 homo sapien
5 mus musculu
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2 human herpe
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## ALIGNMENTS

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01-FEB-1996;
01-FEB-1996;
30-MAY-2000;
                                                                                    STRAIN-NEW ZEALAND WHITE: TISSUE-OVARY;
MEDLINE-93286072; PubMed-7685342;
Lee V.H., Schwoebel E.D., Prasad S.V., Cheung P
Cook R.G., Dunbar B.S.;
"Identification and structural characterization
                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ZONA PELLUCIDA SPERM-BINDING PROTEIN 2 (ZONA 2PP2) (ZONA PELLUCIDA PROTEIN A) (75 KDA ZONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                              zona pellucida protein.";
J. Biol. Chem. 268:12412-12417(1993).
                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Vibrio cholerae produces a s intestinal tight junctions."; Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                     (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                             FCIGRLCVQDGFVT
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М.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaper J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cad. Sci. U.S.A. 88:5242-5246(1991).
INCREASES THE PERMEABILITY OF THE SMALL
ING THE STRUCTURE OF INTERCELLULAR TIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽,
                                                                                                                                                                                                                                                                                                                                            STANDARD;
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V -> A (IN STRAINS 569B AND 86015)
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V -> A (IN STRAIN 569B).
A -> S (IN STRAIN 86015).
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Pred.
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                                                                                                                                                                                                 Leporidae;
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                                                                                                                                                                                                                                                                                                                                            666
                                                                                                                                                                                                             Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                            ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                         75-kDa rabbit
                                                                                                                                                                                                                                                                PROTEIN)
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RESULT 3
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Best Local S
Matches 7
[2]
SEQUENCE FROM N.A.
MEDLINE-99425270; PubMed-10493829;
Loftus B.J., Kim U.-J., Sneddon V.P.
Loftus Mason T., Crosby M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
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Q05996;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
20NA PELLUCIDA SPERM-BINDING PROTEIN 2 PRECURSOR
6LYCOPROTEIN ZP2) (ZONA PELLUCIDA PROTEIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix.
NON_TER 1
CHAIN <1 66
                                                            Dev.
                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                      Liang L.-F., Dean J.;
"Conservation of mammalian secondary
promoter of the human gene to function
                                                                                                    MEDLINE=93215931;
                                                                                                              TISSUE-Ovary
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Sulfatation; Sperm; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00100; zona_pellucida; PROSITE; PS00682; ZP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L12167; AAA31502.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PROTEOLYTICALLY CLEAVED AFTER FERTILIZATION, AND THIMODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO POLYSPERITM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                     GELCTQDGFM
                                                            Biol.
                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conser
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637
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318
318
73
126
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613
                                                           156:399-408(1993).
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                        (Human).
                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                   PubMed=8385033;
                                                                                                                                                    Chordata;
Primates;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZONA PELLUCIDA SPERM-BINDING EXTRACELLULAR (POTENTIAL).
                                                                    function in mouse occytes."
                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                     PRT;
                   V.P.,
                                                                                                                                                                                                                                                                                                                                                                                             D6C8E2BA2D21020B
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(GLCNAC...)
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                   Kalush
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          Brandon, Cronin
                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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(POTENTIAL)...)
(POTENTIAL)...)
(POTENTIAL)...)
(POTENTIAL)...)
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Barnstead

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RESULT 4
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Best Local S
Matches 7
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077726;
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or send a
               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
20NA PELLUCIDA SPERM-BINDING PROTEIN 2 PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP2) (ZONA PELLUCIDA PROTEIN A).
                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. Then use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00100; zona_pellucida; PRINTS; PR00023; ZPELLUCIDA. PROSITE; PS00682; ZP_DOMAIN; 1. Glycoprotein; Signal; Sulfatati
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00100;
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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MIM; 182888; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M90366; AAA61335.1; -. EMBL; AF001550; AAB67599.1;
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Macaca
                                                                                                                                     369 GELCTQDGFM
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nes 7; Conserv
                                                                                                                                                  4 GRLCVQDGFV 13
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DEVELOPMENTAL STAGE: EXPRESSED DURING THE 2-WEEK OOCENESIS, PRIOR TO OVULATION.

PTM: IS ROTEOLYTICALLY CLEAVED AFTER FERTILIZATI PRODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSAC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 ZP DOMAIN.
radiata (Bonnet monkey)
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39
717
737
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                                                                                   STANDARD;
                                                                                                                                      378
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                                                                                                                                                                                       54.48;
70.08;
                                                                                                                                                                                                                                                                                                                                                                               Sulfatation;
                                                                                                                                                                                                                                ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu R.X., Kang H.-L., Mitchell Venter J.C., Adams M.D.; ther features in 12 Mb of DNA s
                                                                                                                                                                                                                            N-LINKED (GLCNAC...) (
CGLCNAC...) (
N-LINKED (GLCNAC...) (
                                                                                                                                                                            Score 43; DB
Pred. No. 6.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                 ZONA PELLUCIDA S
EXTRACELLULAR (I
POTENTIAL.
CYTOPLASMIC (POT
                                                                                                                                                                              ۲;
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                               Sperm; Receptor; Transmembrane;
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                                                                                  745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                       A SPERM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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CROSS-LINKED
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                                                                                                                                                                                                Length 745;
                                                                                                                                                                                                                                CRC64;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR
                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TION, AND THIS
MAY PLAY AN
POLYSPERMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROWTH PHASE
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RESULT 5
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Best Local
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         YBGK_HAEIN
P44298;
01-NOV-1995
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoprotein-zp2.";

Mol. Reprod. Dev. 50:229-239(1998),

FUNCTION: Zp2 FORMS WITH Zp1 AND Zp3 THE ZONA PELLUCIDA,

WHICH Zp2 AND Zp3 COMPLEX INTO COPOLYMERS CROSS-LINKED B:

Zp2 ACTS AS A SECONDARY SPERM RECEPTOR.

FINE SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jethanandani P., Santhanam R., Gupta S.K.;
"Molecular cloning and expression in Escherichia coli
encoding bonnet monkey (Macaca radiata) zona pellucida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; NCBI_TaxID=9548; [1]
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                             Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y10690; CAA71693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98250422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                     369
                                                                                                                                          4 GRLCVQDGFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: IS PROTEOLYTICALLY CLEAVED AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATRIX
                                                                                                                    GELCTODGFM
                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00100;
                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        PR00023; ZPELLUCIDA.
; PS00682; ZP_DOMAIN; 1.
otein; Signal; Sulfatati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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(Rel.
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310
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                                                           STANDARD;
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           32,
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                                                                                                                                                                                                                                       38
745
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745
105
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269
                                                                                                                                                                                                                           82710
                                                                                                                                                                            54.4%;
           Last sequence update)
Last annotation updat
                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                        Sulfatation;
                                                                                                                                                                                                                           ₩;
                                                                                                                                                                                                                        N-LINKED (GLCNAC...
                                                                                                                                                                           Score 43; DB
Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                      ZONA PELLUCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
                                                           PRT;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Sperm; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.K.;
Escherichia coli of cDNA
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                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      SPERM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIGOSACCHARIDES
                                                                                                                                                                                        Length 745;
                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                 Indels
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(POTENTIAL).
(POTENTIAL).
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POLYSPERMY
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                              ZP2_CANFA STANDARD; PRT; 715 AA. PA7983; PA7983; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) O1-FEB-1996 (Rel. 33, Last annotation update) CONA PELLUCIDA SPERM-BINDING PROTEIN 2 PRECURSOR CLYCOPROTEIN ZPZ) (ZONA PELLUCIDA PROTEIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9535630; PubMed-7542800;
MEDLINE-9535630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Felschmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavege A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995).
-I- SIMILARITY: STRONG, TO E.COLI YBGK.
-I- SIMILARITY: TO B.SUBTILIS YCSJ AND YEAST UREA AMIDOLYASE (DUR1,2).
    SEQUENCE FROM TISSUE-Ovary;
                                                                            a variety
                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Canis familiaris (Dog).
Chordata; Craniata; Vertebrata;
Cranidae;
                                                                                                                                                                                                                                                                                                                    ZP2 OR ZPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32845;
TIGR; HI1730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
STRAIN-RD / KV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; P.
Haemophilus
                                                                                                                       Sacco A.G.;
                                                                                                                                                        MEDLINE-95143578;
                                                                                                                                                                                TISSUE-Ovary;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae.
                                                                                                                                       Harris J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 80.0
8; Conservative
                                                           and characterization of zona pellucida y of mammalian species: the ZPA, ZPB and 4:361-393(1994).
                                                                                                                               D., Hibler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
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/ KW20 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein.
309 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC23376.1; -.
                                                                                                                                     PubMed=7841460;
er D.W., Fontenot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34562 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB
Pred. No. 6.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                       G.K.,
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3;
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                                                                                                                                       K.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 309
                                                                              genes and delighted 2PC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.A., Kirkness E.F., y B.A., Merrick J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64
                                                                                                                                                                                                                                                                                                                                                             (ZONA PELLUCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                         Yurewicz
                                                                                                                                                                                                                                                            Canis
                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                cDNAs from
families.";
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CARBOHYD
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                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00682; ZP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00100; zona_pellucida; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U05779; AAA74386.1; -. EMBL; D45069; BAA08097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okazaki Y., Isojima S., Sugimoto M.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okazaki Y.,
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001507; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
   715
                                                                                                                                                                    39
685
706
367
367
193
220
266
321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Sulfatation; Sperm; Receptor; Transmembrane;
   AA;
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715
684
705
715
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220
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79938
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N-LINKED
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R -> A (II
L -> P (II
S -> A (I
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R -> A (IN REF. 2) (
L -> P (IN REF. 2) (
L -> P (IN REF. 2) (
S -> A (IN REF. 2) 
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                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
POTENTIAL.
508D6DE804F4DC5C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELLUCIDA
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                                                                                                                                                                                                        (POTENTIAL)
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RESULT TELCA
                                                                                                                                                                         Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
 TISSUE=Ovary;
Okazaki Y., I
                                                        a variety
                                                                                Sacco A.G
                       SEQUENCE FROM N.A.
                                                                    "Cloning and
                                                                                          Harris J.D.,
                                                                                                      MEDLINE=95143578;
                                                                                                                   TISSUE=Ovary;
                                                                                                                             SEQUENCE FROM
                                                                                                                                                   NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                          7
                                             y of mammalian sp
4:361-393(1994).
Isojima
                                                        characterization of zona pellucida mammalian species: the ZPA, ZPB and
                                                                                            Hibler
                                                                                                                             N.A.
                                                                                          PubMed=7841460;
er D.W., Fontenot G.K.,
 s,
 Sugimoto
 3
                                                                                          Hsu K.T.,
                                                         and
                                                        genes and cDNAs from ZPC gene families.";
                                                                                                                                                                                                                        (ZONA
                                                                                            Yurewicz E.C.,
                                                                                                                                                                Euteleostomi; Felis.
                                                                                                                                                                                                                         PELLUCIDA
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RESULT E
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Best Loc
Matches
                                                                                                                                                                                                                                                          01-FEB-1991
01-FEB-1991
30-MAY-2000
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SEQUENCE
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TRANSMEM
                                                                                                                                                                                                                                                                                                                   ZP2_MOUSE
P20239;
                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                       GLYCOPROTEIN ZP2) (ZONA ZP2 OR ZP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0023; ZPELLUCIDA.
PROSITE; PS00682; ZP_DOMAIN; 1.
Glycoprotein; Signal; Sulfatati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U05776; AAA74388.1; -. EMBL; D45067; BAA08095.1; -. InterPro; IPR001507; -.
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entities requires a license
or send an email to license
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-I- FUNCTION: ZP2 FORMS WITH ZP1 AND ZP3 THE ZONA PELLU
WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINI
ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRI
   Liang L.-F., Chamow S.M., "Oocyte-specific expression of the zona pellucida gen
                                                    MEDLINE-90205829; PubMed-1690843;
                                                                           TISSUE-Ovary;
                                                                                                                                                                                                                                           ZONA PELLUCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00100; zona_pellucida; 1.
                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                           368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GRLCVQDGFV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                 musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                      8
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES
                                                                                                                                                                                                               (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 39, Last annotation update)
(IDA SPERM-BINDING PROTEIN 2 PRECURSOR
   cific expression of pellucida genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39
687
708
369
369
87
96
2222
2222
268
397
483
716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matrix.
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                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
696
696
707
707
716
636
87
222
258
268
531
531
483
637
80135
                                                                                                                                                   Chordata;
Rodentia;
                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfatation; Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 98
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW;
                                       Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POT

V -> G (IN REF. 2).

L -> P (IN REF. 2).

F -> S (IN REF. 2).

GC5745496E82CB671 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB Pred. No. 14; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZONA PELLUCIDA SPERM-BINDI EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). ZP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВY
                                                                                                                                             Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                    PRT;
                        mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                              õ
                                                                                            35-50
                  Zp-2: developmental regulation
                                                                                                                                                                                                                                                                                                                                  713
                                                                                                                                                                                                                                                                                                                                  B
                                                                                              AND
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S CROSS-LINKED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 716;
                                                                                                                                                                                                                                         (ZONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                    Euteleostomi,
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                                                                                                                                                 Murinae;
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                                                                                                                                                                                                                                         PELLUCIDA
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Y ZP1.
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                                                                                                                                                                15-DEC-1998
15-DEC-1998
15-DEC-1998
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SEQUENCE FROM N.A. MEDLINE-96335691;
                                                    Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Muromegalovirus.
NCBI_TaxID=79700;
                                                                                                                                               DNA
                                                                                                                                                                                                                                                          RCMVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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                                                                                                           Rat cytomegalovirus (strain Maastricht)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                             -DEC-1998 (Rel. 3
-DEC-1998 (Rel. 3
-DEC-1998 (Rel. 3
-POLYMERASE (EC
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(EC

PubMed=8757999

37, Created)
37, Last sequence update)
37, Last annotation updat
C 2.7.7.7).

update)

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Herpesviridae;

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Query Match
Best Local
                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
DPOL_RCMVM
Q85428;
                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A34782; A34782.
MGD; MGI:99214; Zp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M34148; AAA40586.1; -. PIR; A34782; A34782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3lycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                               Local
                                                                                                                              3 IGRLCVQDGFV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Cell. Biol. 10:1507-1515(1990).

FUNCTION: ZP2 FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA,
WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED B:
ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PROTEOLYTICALLY CLEAVED AFTER FERTILIZATION, AND THIS MODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY AN IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO POLYSPERMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: OOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OOGENESIS, PRIOR TO OVULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM:
                                                                                                 IDELCAODGFM 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00100; zona_pellucida; 1.
'S; PR00023; ZPELLUCIDA.
'TE; PS00682; ZP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                              Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99214; Zp2.
IPR001507; -
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Sulfatation;
                                                                                                                                                                                                                                                Ą,
                 STANDARD;
                                                                                                                                                                                                                                         34
713
683
703
703
630
630
83
172
114
217
264
393
80209
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                                                                                                                                                                               50.
63.
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N-LINKED
N-LINKED
                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                             ZONA PELLUCIDA SPERM-BINDING EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
DCF9AE6CCD3461EF CI
                 PRT;
                                                                                                                                                                Mismatches
                                                                                                                                                                                          40;
                                                                                                                                                                               <del>8</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sperm; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DURING
                 1120 AA
                                                                                                                                                                            DB
21;
                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE 2-WEEK GROWTH PHASE
                                                                                                                                                                                               1:
                                                                                                                                                              <u>ω</u>
                                                                                                                                                                                           Length 713;
                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                 (POTENTIAL)
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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                                      the European Bioinformatics Institute.

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modified and this statement is not remove
entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                         Schmidt I., Skinner M.A., Siddell S.G.;

"Nucleotide sequence of the gene encoding the surfaglycoprotein of coronavirus MHV-JHM.";

J. Gen. Virol. 68:47-56(1987).

-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BII-
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MAND IN SYNCYTION FORWATION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                             VGL2_CVMJH STANDARD; PRT; 1235 AA.
p11225;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)
[CONTAINS: SPIKE PROTEIN S1 (90B); SPIKE PROTEIN S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; DNA-directed DNA polymerase; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00136; DNA_POL_B; 1.
PRINTS; PR00106; DNAPOLB.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus.
J. Gen. Virol. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beuken E., Slobbe R., Bruggeman C.A., Vink C.; "Cloning and sequence analysis of the genes encoding I glycoprotein B, ICP18.5 and major DNA-binding protein
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U50550; AAC56433.1; -. InterPro; IPR002064; -.
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                                                                                                                                                                                                                                                                MEDLINE-87111467; PubMed-3027248; Schmidt I., Skinner M.A., Siddell S.G.;
                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA
Coronaviridae;
                                                                                                                                                                                                                                                                                                                                        Murine coronavirus MHV (strain JHM).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
                                                                                                                   between
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 IGRLCVQDG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss Institute of Bioinformatics and the EMBL outsit
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N PYROPHOSPHATE + DNA(N).
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGKYCVQDG
X04797;
D00093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Nuclear protein.
1120 AA; 124853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 CAA28484.1;
BAA00057.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500
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                                                                        is not removed.
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Pred. No.
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Mismatches
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                                                                                  There are no rest
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                                                                                                                                                                                                                                                                                                                                                       DNA
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ng protein of
                                                                                                                                                                                         THE BINDING ED IN MEMBRAN
                                                                        Usage
                                                                                                                                                                                                                                                   surface
                                                                                                                                                                                                                                                                                                                                                       stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1120;
                                                                                                                                                                                           BINDING OF VIRIO MEMBRANE FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                         Ьy
                                                                                                     restrictions
                                                                                                                                                                                                                                                  projection
                                                                         and
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rat
                                                                                                                      EMBL outstation
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                                                                                                                                  collaboration
                                                                         in no way
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VGL2_CVMA5
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                                                                                                                                                                                                             VGLZ_CVMA5 STANDARD; PKKI; LULL PB11224; P11224; O1-JUL-1989 (Rel. 11, Created) O1-FEB-1996 (Rel. 33, Last sequence update) O1-FEB-1996 (Rel. 33, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) E2 GLYCOPROTEIN PREGURSOR (SPIKE GLYCOPROTEIN) E2 GLYCOPROTEIN S1 (90B); SPIKE PROTE
                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
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CARBOHYD
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TRANSMEM
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Envelope SIGNAL 1 10
                                             Luytjes W., Sturman L.S., Bredenbeek P.J., Charite J., van der Zeijst B.A.M., Horzinek M.C., Spaan W.J.M.; "Primary structure of the glycoprotein £2 of coronavirus identification of the trypsin cleavage site."; Virology 161:479-487(1987).

-i- FUNCTION: THE PEPFLOMER PROTEIN MEDIATES THE BINDING TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRAN AND IN SYNCYTIOM FORMATION.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                           Viruses; ssRNA positive-strand Coronaviridae; Coronavirus. NCBI_TaxID-11142;
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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the
                           This
                                                                                                                                  MEDLINE=88072088; PubMed=2825419;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                          Murine coronavirus MHV (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002552;
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                   between
                                                                                                                                                                                                                                                                                                                  762 CIGSTCAEDG
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s SWISS-PROT entry is copyright. It is produ-
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
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SPIKE PROTEIN S2.
EXTRACELLULAR (PC
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CYTOPLASMIC
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E2 GLYCOPROTEIN.
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VGL2_CVM4

ID VGL2_CVM4

ID VGL2_CVM4

STANDAME

AC P22432;

AC P22432;

DT 01-AUG-1991 (Rel. 19, Created)

DT 15-JUL-1999 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 22 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)

CONTAINS: SPIKE PROTEIN S1 (90B); SPIKE PROTEIN S2 (90A)].

""" / STITAIN wild type 4) (MHV-4).
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                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-90085815; PubMed-2556846;

Parker S.E., Gallagher T.M., Buchmeler M.J.;

Parker S.E., Gallagher T.M., Buchmeler M.J.;
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CARBOHYD
                                                       SEQUENCE FROM N.A.
MEDLINE-91353381; PubMed-19
Parker S.E., Buchmeier M.J
                                                                                                                              "Sequence analysis reveals extensive delettions within the E2 glycoprotein murine hepatitis virus."; Virology 173:664-673(1989).
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Pfam; PF01601; Corona_S2;
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SPIKE PROTEIN S1.
SPIKE PROTEIN S1.
SPIKE PROTEIN S1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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Pred. No.
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VGL2_CVMJC
STANDARD; PKT;
ID VGL2_CVMJC
STANDARD; PKT;
AC Q02385;
AC Q02385;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-UTL-1999 (Rel. 38, Last annotation update)
DE 22 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)
DE 22 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN S2 (90A)].
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903 CIGSTCAEDG 2 CIGRLCVQDG 11

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Similarity 6; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "RNA sequence analysis of the E2 genes of wildtype and neuroattenuated mutants of HMV-4 reveals a hypervariable Adv. Exp. Med. Biol. 276:395-402(1990).

-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: NEARLY IDENTICAL TO THE E2 GLYCOPROTEINS AND MVH-A59 STRAIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                  N-LINKED (GLCNAC...)
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SPIKE PROTEIN S1.
SPIKE PROTEIN S2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
Pred. No. 39;
1; Mismatches
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                                                                                                                                                           GELCNAC.
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                                      Length 1376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine coronavirus MHV (strain JHMV / variant CL-2).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID-33735;
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Pfam; PF01601; Corona_S2;
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Local Similarity 60.0
hes 6; Conservative
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CONFLICT 37
CONFLICT 41
CONFLICT 68
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CONFLICT 80
SEQUENCE 87 AA; 9
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40S RIBOSOMAL PROTEIN S21 (S28).
RPS21 OR SPBC18E5.06.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete:
Eukaryota; Fungi; Ascomycota; Schizosaccharomyceteese;
                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRE
(GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE)
  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-ELDER / ATCC 33958; MEDLINE-95142655; PubMed-7840643;
                                                        Chryseobacterium.
NCBI_TaxID=238;
                                                                                    Flavobacterium meningosepticum.
Bacteria; CFB group; Flavobacteria; Flavobacteriaceae;
                                                                                                                                                                                                    ASPG_FLAME
Q47898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae and its counterparts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86104253; PubMed-3910104;
Itoh T., Otaka E., Matsui K.A.;
"Primary structures of ribosomal
                                                                                                                GLUCOSAMINYL) -L-ASPARAGINE AMIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01
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PS00996; RIBOSOMAL_S21E; 1.
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PROTEIN S21 (S28).
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ota; Schizosaccharomycetes;
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C -> A (IN REF. 1)

A -> O (IN REF. 1)

C -> D (IN REF. 1)

T -> Q (IN REF. 1)

E -> T (IN REF. 1)

970F7B10DC348B6A C
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SE) (N4-(N-ACETYL-BETA-
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Search completed: June 13, 2001, 14:30:39 Job time: 529 sec
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Best Local Similarity 66.7
Matches 6; Conservative
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Protein SCI. 7:774-781(1998).

-I- EUNCTION: CLEAVES THE GLCNAC-ASN BOND WHICH JOINS OLIGOSACCHARIDES TO THE PEPTIDE OF ASPARAGINE-LINKED GLYCOPROTEINS. REQUIRES THAT THE GLYCOSYLATED ASPARAGINE MOIETY IS NOT SUBSTITUTED ON ITS AMINO (R1) AND CARBOXYL (R2) TERMINUS.

-I- CATALYTIC ACTIVITY: N4-(BETA -N-ACETYL-D-GLUCOSAMINYL)-L-ASPARAGINE + H(2)O - N-ACETYL-BETA-GLUCOSAMINYLAMINE + L-ASPARTATE.

-I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAINS.

-I- SUBCELLULAR LOCATION: PERIPLASMIC.

-I- SUBCELLULAR LOCATION: PERIPLASMIC.
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MEDLINE-98200483; PubMed-9541410;

XUAN J., Tarentino A.L., Grimwood B.G., Plummer T.H. Jr., Cui T
Guan C., van Roey P.;

"Crystal structure of glycosylasparaginase from Flavobacterium
meningosepticum.";
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MEDLINE-94071939; PubMed-8250923;

Tarentino A.L., Plunmer T.H. Jr.;

"The first demonstration of a procaryotic glycosylasparaginase.";

Blochem. Blophys. Res. Commun. 197:179-186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and sequence analysis of Flavobacterium meningosepticum glycosylasparaginase: a single gene encodes the alpha and beta subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Hydrolase;
SIGNAL 1
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Pred. No. 15;
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O14424 coccidioide
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O21801 caenorhabdi
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Ogt087 arabidopsis
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Q973v6 vibrio chol
Q917q6 vibrio chol
Q91c5 arabidopsis
Q9kyg6 streptomyce
Q22208 caenorhabdi
Q9zq11 arabidopsis
Q9ya16 aeropyrum p
Q9z919 chlamydia p
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porcine		Q9ifi6 porcine cyt	Q9ua44 aplysia cal	Q914n2 streptococc		059088 pyrococcus	P90594 trypanosoma		Q18925 caenorhabdi	Q14964 homo sapien	Q9sj18 arabidopsis		Q9vis5 drosophila	~	P87241 schizosacch	P72738 synechocyst		094496 schizosacch	vibr		homo sap		murine	murine	Q9wr70 murine hepa

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Infect. Immun. 68:1507-1513(2000).
EMBL; AF207857; AAF40142.1; -.
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                                                                                                                                                                                                                                                                                                 Vibrio mimicus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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STRAIN-EL TOR N16561 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Colll S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., W
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
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rstA(RstA), rstB(RstB), cep(Cep),
genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shin H.J., Park Y.C., Kim Y.C.; "Cloning and nucleotide sequence analysis of the virulence cassette from vibrio cholerae KNIH002 isolated in Korea."; Misainmurhag Hoiji 35:205-210(1999).
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Vibrio cholerae.
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EMBL; AF175708; AAD51358.1;
EMBL; AF123049; AAD26854.1;
EMBL; AE004224; AAF94615.1;
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                  Bentley S. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudioctyledons; core eud
Brassicales; Brassicaceae; Arabidopsis.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
7. 2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                Submitted (NOV-1995) to the ENEMBL; U40028; AAA81120.1; -. SEQUENCE 256 AA; 26045 MW;
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Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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Redenbach M., Kleser H.M., Denapaite D.
Redenbach M., Kleser H.M., Denapaite D.
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detaile
"he 8 Mb Streptomyces coellcolor A3(2)
Mol. Microbiol 21:77-96(1996).
EMBL, AL356595; CAB92272.1; -
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T13E11.8 PROTEIN.
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Q9YAL6;
01-NOV-1999
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"Arabidopsis thaliana chromosome II BAC T13E11 ger submitted (FEB-199) to the EMBL/GenBank/DDBJ data EMBL; AC006217; AAD15523.1; -.

SEQUENCE 263 AA; 29788 MW; F3DB9F4E7BA75B6D CF
                                                                                                                                                                                                    Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                EMBL; AP000062; BAA80932.1;
                                                                                                                                                                                                                                                                      crenarchaeon, Aeropyrum pernix DNA Res. 6:83-101(1999).
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haik
Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., K
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y
Tamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K.,
Nomura N., Sako Y., Kikuchi H.;
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STRAIN-CV. COLUMBIA;
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118
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, 15.8 KDA PROTEIN APE1926.
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A White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
A Berry K., Bass S., Linher K., Weldman J., Khouri H., Craven B.,
A Bowman C., Dodson R., Gwinn M., Nelson W., Deboy R., Kolonay J.,
A McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
T pneumoniae AR39.";
L Nucleic Acids Res. 28:1397-1406(2000).
R PMBL; AB0002545; BAA93375.1; -.
R EMBL; AB002518; AAF38422.1; -.
R TIGR; CP0606; -.
R TIGR; CP06165; -.
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Best Local Similarity
Matches 7; Conser
                                                                                                                        01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-OCT-2000 (TremBLrel. 15, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1).
                       Campylobacter.
                                                Bacteria;
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01-OCT-2000
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MEDLINE-99206606; PubMed=10192388;

MEDLINE-99206606; PubMed=10192388;

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

Nat. Genet. 21:385-389(1999).
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01-MAY 1999 (TrEMBLrel 10, Last sequence update)
01-OCT-2000 (TrEMBLrel 15, Last annotation updat)
HYPOTHETICAL 23.0 KDA PROTEIN.
CPN0165 OR CPJ0155 OR CP0606.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydoph
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SEQUENCE 1
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195 AA; )
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                                        Campylobacter group;
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i H., Craven B.,
y R., Kolonay J.,
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-129SY; TISSUE-TESTES;

Pan Y., Decker W.K., Hug A.H.H.M., Craigen W.J.;

"Retrotransposition of glycerol kinase-related genes from the X chromosome to autosomes: Functional and evolutionary aspects.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF117733; AAD24550.1; -.

HSSP; P08859; IGLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCEROL KINASE-LIKE PROTEIN 1.

GK-RS1 OR GKRS1.

MUS miscritic
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O9WU64;
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
O1-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
PROSITE; PS00933; FGGY_KINASES_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";

Rature 403:65-668(2000).

EMBL; AL139078; CAB73945.1; -.

INTERPRO; IPRO0728; -.

INTERPRO; IPRO02086; -.

PEAM; PEO0586; AIRS; 1.

PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.

PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:891990; Gk-rs1.
INTERPRO; IPR000577; -.
INTERPRO; IPR002086; -.
IPFAM; PF00370; FGGY; 1.
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karleyshev A., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
STRAIN-NCTC 11168;
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VGQLCLQDG
                             IGRLCVQDG
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273
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                                                                                                                                                                                                                                    59871 MW;
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                                                                                                  Score 41; DB pred. No. 32; 3; Mismatches
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Pred. No.
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                                                                                                                                                     11;
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069514;

01-AUG-1998 (TrE

01-AUG-1998 (TrE

01-JUN-2000 (TrE

DNA POLYMERASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL: AL023596; CAA19155.1; -.
                                                                                                                                                                                                          Coccidioldes immitis.
Eukaryota; Fungl; Asc
Coccidioldes.
                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAY-2000 (TrEMBLrel. 13,
BETA-GLUCOSIDASE (EC 3.2.1.2
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Seeger K., Harris D.;
Submitted (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                    INTERPRO; IPR001764;
INTERPRO; IPR002772;
INTERPRO; IPR002772;
INTERPRO; IPR00233; Glyco_hydro_3; 1.
PFAM; PF01915; Glyco_hydro_3_C; 1.
PRINTS; PR00133; GLHYDRLASE3.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3;
                                                                                                                                  Yu J.-J., Thomas P.W., Seshan K., Submitted (JAN-1997) to the EMBL/CEMBL; 087805; AAB57972.1; -.
                                                                                                                                                                                                                                                                                               014424;
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MEDLINE=93188700; PubMed=8446027;
Eiglmeier K., Honore N., Woods S.A.,
"Use of an ordered cosmid library to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Barrell
Submitted (MAY-1998)
                                                                                                                                                                   STRAIN-C735;
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                                                                                                                                                                                                NCBI_TaxID=5501;
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                                                    Hydrolase;
SEQUENCE
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6; Conserv
 Similarity
8; Conserv
                                                   Glycosidase.
870 AA; 95467 MW;
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nilarity 54.5%;
Conservative
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  Conservative
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e EMBL/GenBank/DDBJ
Score 41; DB Pred. No. 49; 1; Mismatches
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Last annotation
GAMMA AND TAU.
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EMBL/GenBank/DDBJ
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01-OCT-2000 (TrEMBLrel. 15, La
T 01-OCT-2000 (TrEMBLrel. 15, La
HYPOTHETICAL 136.8 KDA PROTTOK17, 260.
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Q9NLK9;
Q9NLK9;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
Q1-CCT-2000 (TrEMBLREL 15, Last annotation update)
WFOOTHETICAL 14.9 KDA PROTEIN (FRAGMENT).
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Eukaryota; Viridiplantae; Embryophyta; Trache;
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                               Hypothetical protein.
NON_TER 138 13
SEQUENCE 138 AA; 1
                                                                                                                                                                                                                                                                                                                                                  Murphy L., Quail M., Harris Submitted (JUL-2000) to the EMBL; AL160493; CAB98051.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
EMBL; AL133977; CAB67633.1; -
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Benes V., Wurmbach E.,
Mayer K.F.X., Quetier I
Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9M2P3
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14866 MW;
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Pred. No. 82;
2; Mismatches
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dicots; Rosidae;
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Search completed: June 13, 2001, 14:29:48 Job time: 549 sec

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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      seq length:
seq length:
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Match Length
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/FCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/laa/backfiles1.pep:*
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      BB
   US-08-624-601-8
US-08-08-453-472-5
US-08-483-952-5
US-08-484-9938-43
US-08-484-158B-43
US-08-486-150A-43
US-08-486-731-43
US-08-486-397-51
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US-08-486-397-64
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Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 43, Appli
Sequence 51, Appli
Sequence 64, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
41	41	41	41	41 .	41	41	41	41	41	41	41	42.5	42.5	42.5	42.5	42.5	42.5
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US-08-149-223A-14	US-08-458-731-14	US-08-480-150A-14	US-08-484-596A-14	US-08-484-158B-14	US-08-484-993B-14	US-08-149-223A-10	US-08-458-731-10	US-08-480-150A-10	US-08-484-596A-10	US-08-484-158B-10	US-08-484-993B-10	US-09-249-448-64	US-09-249-461-64	US-08-809-455-64	US-09-249-451-64	US-09-249-472-64	US-09-249-471-64
Sequence 14	Sequence 14	Sequence 14	Sequence 14	Sequence 14	Sequence 14	Sequence 10	Sequence 10	Sequence 10	Sequence 10	Sequence 10	Sequence 10	Sequence 64					
, Appl	i, Appl	i, Appl	, Appl	`	`	•	•	•	•	•	•	`	`	-	•	`	, Appl

RESULT

ALIGNMENTS

## COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/624,601 FILING DATE: 08-APR-1996 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Schneller Dr., John W. REGISTRATION NUMBER: 26,031 REFERENCE/DOCKET NUMBER: BAMCZ0019P2 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)414-4040 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARRCTERISTICS: LENGTH: 400 amino acids TYLET : milo acids US-08-624-601-8 US-08-624-601-8 ; Sequence 8, Applicatio ; Patent No. 5882653 ; GENERAL INFORMATION: APPLICANT: Kaper Dr., James B. APPLICANT: Levine Dr., Myron M. APPLICANT: Levine Dr., Myron M. TITLE OF INVENTION: Vibrio cohlerae Ol (CVD111) and non-Ol TITLE OF INVENTION: (CVD112 and CVD112RM) serogroup vaccine strains, methods TITLE OF INVENTION: of making same and products thereof NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk IMMEDIATE SOURCE: CLONE: zot MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ADDRESSEE: Spence: STREET: 1100 New ' CITY: Washington STATE: D.C. COUNTRY: USA ORGANISM: Vibrio cholerae STRAIN: El Tor 7946 STRANDEDNESS: TYPE: amino acid TOPOLOGY: 20005 Application US/08624601 E: Spencer & Frank 1100 New York Ave. N.W. linear Suite 300

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US-08-453-472-5
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Best Local
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                                                                                                                                                                                                                                                                             TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/453,472
FILING DATE: 30-May-1995
CLASSIFICATION: 435
CRISTICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,948
APPLICATION NUMBER: US 08/038,948
FILING DATE: 26-MAR-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:

OR 107/030,462
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/930,462
APPLICATION DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379
APPLICATION NUMBER: US 07/364,379
ATTORNEY_AGENT. INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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ADDRESSEE: MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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NAME/KEY:
                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                               INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE:
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14; Conservative
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100.0%; Pred. No. 9.7e-06;
tive 0; Mismatches 0;
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RESULT

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; IDENTIFICATION METHOD:
; OTHER INFORMATION: human ZP2 protein
US-08-453-472-5
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Best Local Similarity
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                                                                                                         ; TOPOLOGY: 11; MOLECULE TYPE: US-08-038-948-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08038948 Patent No. 5641487
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/930,462
APPLICATION DUBBER: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/364,379
APPLICATION NUMBER: US 07/364,379
APPLICATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
                               Matches
                                             Query Match
Best Local
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
SOFTMARE: Patentin Release
APPLICATION NUMBER: US/08/038,948
FILING DATE: 26-MAR-1993
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 99:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 20005-3918
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                                                                                                                                                           STRANDEDNESS
4 GRLCVQDGFV 13
                                                                                                                                                                                          ENGTH:
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                              l Similarity
7; Conserv
                                                                                                                                                                           amino acid
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1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                         745 amino acids
                               Conservative
                                                                                                                                          ss: single
linear
                                                                                                                           protein
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70.0%;
                                                54.4%;
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                                                                                                                                                                                                                                                                                                        99152/E-266-88/2
                                 Score 43; DB 1;
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                    Length 745;
                                      Indels
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Best Local
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tent No. 5672488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DEAN, JUF
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-JUN-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 101
                                                                                                                                             IDENTIFICATION METHOD:
OTHER INFORMATION: human ZP2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/930,462 FILING DATE: 20-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/453,952 FILING DATE: 30-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/364,379 FILING DATE: 12-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                LOCATION:
                                                                                                                                                                                              NAME/KEY: 2P2
                                                                                                                                                                                                                                                                               TISSUE TYPE:
                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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 4 GRLCVQDGFV 13
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                                                Similarity
7; Conserv
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                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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SYSTEM: PC-DOS/MS-DOS
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                                                               54.48;
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BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
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                                               Score 43; DB:
Pred. No. 16;
1; Mismatches
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                                                                                Length 745;
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US-08-862-903-5
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; MOLECULE TYPE:
US-08-484-993B-43
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                                                                                                                          Sequence 5, Application US/08862903 Patent No. 5916768
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                                                                                              GENERAL INFORMATION: APPLICANT: DEAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                 TITLE OF INVENTION: CONTRACEPTIVE VACCINE
TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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o. 5837497
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                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                      745 amino acids
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Podolski, Joseph S.

VENTION: Materials and Methods for Immunocontraception
                                                                                              DEAN, JURRIEN
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                           linear
MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                           54.4%;
70.0%;
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                                                                                                                                                                                                                                                                                          1; Mismatches
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Indels

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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: human ZP2 protein
US-08-862-903-5
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                                                                                 US-08-484-158B-43
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FILING DATE: 26-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/930,462
FILING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/364,379
FILING DATE: 12-JUN-1989
ATTORNEY/ACENT INFORMATION:
                                      Sequence 43, Applicat Patent No. 5976545 GENERAL INFORMATION:
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/
SOSTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
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                          APPLICANT:
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                                                                                                                                          369
                                                                                                                                       4 GRLCVQDGFV 13
| || ||||:
369 GELCTQDGFM 378
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                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                             NAME/KEY: ZP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GANISM:
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                                                                                                                                                                                                 Similarity 70.07; Conservative
                                                    3, Application US/08484158B 5976545
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Harris Ph.D., Jeffrey D.
Hsu, Kuang T.
Podolski, Joseph S.
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30-May-1995
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                                                                                                                                                                                                    Score 43; DB 2; Pred. No. 16; 1; Mismatches
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US-08-484-596A-43
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                            Sequence 43, Application US/08484596A Patent No. 5981228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN REL
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 07-JUNE-9
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-NOV-93
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION UNDATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/9:
FILING DATE: 09-NOV-92
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELLEFAX: 25-3856
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                               APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                             369 GELCTODGFM 378
                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/149,223 FILING DATE: 09-NOV-93
COMPUTER READABLE FORM:
                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                               4 GRLCVQDGFV 13
               COUNTRY: United States of America ZIP: 60606-6402
                                                 STATE:
                                                              CITY: Chicago
                                                                            ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60606-6402
                                                                                                                                                                                                                 INFORMATION:
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                                              Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                              Harris Ph.D., Jeffrey D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUNE-95
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                                                                                                                                                                                                                                                                                                                                                                                                                    54.4%;
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Pred. No. 16;
1; Mismatches
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                                                                                     Gerstein, Murray & South Wacker Drive
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MEDIUM TYPE:

Floppy disk

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US-08-480-150A-43; Sequence 43, Application US/08480150A; Patent No. 5989550...
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Best Local S
Matches 7
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FILING DATE: 11-WOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973
APPLICATION NUMBER: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clouch David in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 745 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,223
FILING DATE: 09-NOV-1993
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEPAX: 312/474-0448
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CITY: Chicago
STATE: Illinoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 GELCTQDGFM 378
                                                                                                APPLICATION NUMBER: US/08/480,150A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 70.0
nes 7; Conservative
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                                                                                                                                                                                                                                                                      ZIP: 60606-6402
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/484,596A FILING DATE:
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                                                                                                                                                                                                                                                                                    Illinois : United States of America
                                                                                                                                                                                                                                                                                                                                                6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                              Marshall, O'Toole, Gerstein, Murray & Borun 00 Sears Tower, 233 South Wacker Drive
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Best Local S
Matches 7
                                          TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/01
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                   REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
                                                                                                                                                                                 APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/458,731 FILING DATE: 09-NOV-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 S
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 GELCTQDGFM 378
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 60606-6402
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                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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    Application US/08458731
6001599

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                                              745 amino acids
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Podolski, Joseph S.
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                                                                                                                                                                                                                                                                                                         08/012,990
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Pred. No.
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South Wacker Drive
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RESULT 12
US-08-465-380-51
; Sequence 51, A
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Best Local Similarity
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                                                                         Вb
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US-08-149-223A-43
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/012,990
EILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/973,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MANUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 GELCTQDGFM 378
                                                                         369 GELCTQDGFM 378
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OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Pelanaming
                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 09-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clough, David W. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GRLCVQDGFV 13
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                                                                                                     4 GRLCVQDGFV 13
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6027727
                                                                                                                                                                                                                                                   amino acid
   Application US/08465380
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Podolski, Jos
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70.0%;
                                                                                                                                                 54.48;
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                                                                                                                                                                                                                                                                                                 43:
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Pred. No.
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                                                                                                                                   1;
                                                                                                                                                 Score 43;
Pred. No.
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                                                                                                                                     Mismatches
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16;
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RESULT 13
US-08-486-397-51
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                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                    Patent No. 5866542
                                                                                                                                                                                      Sequence 51,
                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: p
ORIGINAL SOURCE:
ORGANISM: Ancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/326,110 FILING DATE: October 18, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                              APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 90071
                                                                                                                                                                                                                                                                        46 CIGRYCYCDEGF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: am TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BIGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/465,380 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                        2 CIGRLCVQD-GF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                       Application US/08486397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 amino acids
                                                                                George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yannick G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                                                                                                                                                                                                                                                                                            53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Gansemans, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,158
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                                                                                                                                                                                                                                                                                                                                                            Score 42.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOS 5.0
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                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                             Gaps
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STREET: 633 WEST E. STREET: Suite 4700

ADDRESSEE:

E: Lyon & Lyon 633 West Fifth Street

CITY: Los Angeles STATE: California

90071

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Best Local Similarity
Thes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Apr-
                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-486-399-51
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                    APPLICANT: Peter W. Ber
TITLE OF INVENTION: NEW
TITLE OF INVENTION: PRO
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/326,111
FILING DATE: October 18, 1994
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CIGRLCVQD-GF 12
||||:|| | | |
46 CIGRVCVCDEGF 57
                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/486,397 FILING DATE: June 5, 1995
                                                                          COUNTRY: U.S.A. ZIP: 90071
                                                                                                            CITY: Los Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (: (213) 955-0440
67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08486399
                                                                                                                                                                                                                                                                                                                       George P. Vlasuk, Patric H. Stanssens, Joris H.L. Mensens, Marc J. Lauwereys Yves R. Laroche, Laurent S. Jespers,
                                                                                                                                                                                                                                                                                   Peter W. Bergum
                                                                                                                                                                                                                                                                                                       Yannick G.J. Gansemans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%;
75.0%;
                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                NEMATODE-EXTRACTED ANTICOAGULANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.5;
Pred. No. 2
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ORIGINAL SOURCE:
ORGANISM: Anc
US-08-486-399-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-461-965-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: June 5, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
                                                                                                                                                                                                                                     ZIP: 90071
COMPUTER READABLE FORM:
FILING DATE: October 18, 1994 ATTORNEY/AGENT INFORMATION: NAME: BIGGS, SUZANNE L.
                                               CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yannick G.J. Gar
APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPOTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 21:
LECOMMUNICATION
                                                                                                 APPLICATION NUMBER: FILING DATE: June
                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                   STREET: 633 West F
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 CIGRVCVCDEGF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CIGRLCVQD-GF 12
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5872098
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                                                                                                                                                                                                                                                                                                                                      E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                 SYSTEM: IBM P.C. Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yannick G.J. Gansemans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yves R. Laroche, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Joris H.L. Mensens, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               George P. Vlasuk, Patric H. Stanssens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ancyclostoma caninum
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                                                                                               June 5, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
75.0%;
                                                 08/326,110
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                                                                                                                 US/08/461,965
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Pred. No. 2.1;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Lauwereys;S. Jespers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 84;
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Page 8
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REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 489-1600
T

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Result
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                             Score
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1: /SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

6: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*

8: /SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS6/gcgdata/geneseq/geneseqp/AA1989.DAT:*

10: /SIDS6/gcgdata/geneseq/geneseqp/AA1989.DAT:*

11: /SIDS6/gcgdata/geneseq/geneseqp/AA1991.DAT:*

12: /SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:*

13: /SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:*

14: /SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT:*

16: /SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

18: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

20: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

22: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

23: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

24: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

25: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

26: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

27: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

28: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

29: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US01-05825A-1
46
1 GRVCVQPG 8
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1.995 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                             Length
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8 2
8 3
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1291
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Y79109
Y79113
Y79117
                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390729
                                                       Peptide antagonist
Peptide antagonist
Peptide antagonist
Peptide antagonist
Peptide antagonist
Encoded by Hepatit
Encoded by Hepatit
                                                                                                                                                                                                                                                                        Description
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<b>σ</b>	3	<b>ω</b>	2	1 3	0	9	8	7 3	6	<b>σ</b>	3	3	2	3	0 3	9 3	8 3	7 3	6 3	<b>5</b> ω	4	ω	23	1 3	0 3	9	80	7 3	6 3	3	3	13 35	2 3
71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	•	•	•		•	•	•	•	•	٠	73.9	•	•	٠	•	•	•	•	•	٠	76.1	76.1
									73																								
																																13	21
Y59870 .	Y59439	W88390	W88388	B41638	G17476	B41718	G17477	B50353	W88389	W88384	Y02927	Y20209	Y79111	Y81461	Y92444	Y92443	Y49567	¥49553	R51500	¥92456	Y92455	Y92454	Y92453	Y92452	Y92451	Y92450	Y92449	Y92448	R05936	W13573	W13574	0	$\mathbf{r}$
normal	delta3	Zneu1	Human 2neul partia	0		Human ORFX ORF1482	Arabidopsis thalia	RinTi	parti		Fragment of human	Human beta-amyloid	-	Human integrin bet	D			endothelial	platelet GP	variant	variant		PIIIa variant	PIIIa variant	PIIIa variant	PIIIa variant Se	PIIIa variant As	a variant I	ed GPII	beta-3	eta-3 inte	occludens	Peptide antagonist

## ALIGNMENTS

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RESULT
Y79105
                                                                              03-AUG-1998;
                                                                                                                  17-FEB-2000
                                                                                                                                                                                                      neuroprotective; dermatological; antiulcer; antiviral;
antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic;
                                                                                                                                                                                                                         Zonulin; antagonist; zonula occludens toxin receptor;
blood-brain barrier; antiinflammatory; cerebroprotect
                                      Fasano A;
                                                                                                  28-JUL-1999;
                                                                                                                                          WO200007609-A1
                                                                                                                                                               Synthetic
                                                                                                                                                                                   gastrointestinal inflammation; therapy.
                                                                                                                                                                                            hypotensive; immunosuppressive;
                                                                                                                                                                                                                                                         Peptide antagonist of zonulin.
                                                                                                                                                                                                                                                                             05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                    Y79105;
                                                                                                                                                                                                                                                                                                                      Y79105 standard; Peptide; 8
                                                           (UYMA-) UNIV MARYLAND BALTIMORE
                                                                              98US-0127815.
                                                                                                  99WO-US16683
                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                              antiparasitic; vasotropic;
                                                                                                                                                                                                                           cerebroprotective;
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Tyrosine phosphata Peptide antagonist Peptide antagonist

WPI; 2000-205565/18

New peptide antagonist of zonulin useful as antiinflammatory agent for

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RESULT
Y79109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TV in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestration, bacterial overgrowth, whipple's diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangictasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, mucosal disease, eosinophille gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; dermatological; antiulcer; antiviral;
antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic;
hypotensive; immunosuppressive; antiparasitic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which bind to a zonula occludens tox
physiologically modulate the opening
                                                                           03-AUG-1998;
                                                                                                                                                28-JUL-1999;
                                                                                                                                                                                                                        17-FEB-2000.
                                                                                                                                                                                                                                                                                                WO200007609-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal inflammation; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide antagonist of zonulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y79109 standard; Peptide; 8
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(UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>_</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grvcvqpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                        98US-0127815.
                                                                                                                                                99WO-US16683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 46; DB 21; 100.0%; Pred. No. 3.2e+05; O. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8;
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B δÃ

28-JUL-1999;

99WO-US16683

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RESULT
Y79113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphanglectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           correction of congenital heart disease with Fontan's operation, mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, ecsinophilic gastroenteritis, and immune diseases. e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This present sequence is that of a peptide antagonist of zonul (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (ZOT) receptor, yet do physiologically modulate the opening of mammalian tight junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 42; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                      Zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotective;
                                                                                                                                                                                                                                                                                                               05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Y79113 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TJ). The peptide antagonists are based on a common and human zonulins, which is believed to be critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-205565/18
                                                                                                           Synthetic
                                                                                                                                                                                   antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic;
                                                                                                                                                                                                  neuroprotective; dermatological; antiulcer; antiviral;
                                                                                                                                                                                                                                                                                                                                                        Y79113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding.
                                                                        WO200007609-A1
                                                                                                                                                             hypotensive; immunosuppressive; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GRVCVQPG 8
                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grlcvqpg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conser
                                                                                                                                                                                                                                                                              antagonist of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              They can be prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.5%;
                                                                                                                                                                                                                                                                                                                                                                                           8
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 21, -
Pred. No. 3.2e+05;
"""" artches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by chemical synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor, yet do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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for receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of zonulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        junctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Query Match
Best Local Similarity
Thehes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc physiologically modulate the opening of mammalian tight junctions (70). The peptide antagonists are based on a common motif of 207 cc and human zonulins, which is believed to be critical for receptor bluding. They can be prepared by chemical synthesis or by use of crecombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal cantinflammation, where they bind to the 207 receptor in the intestine cand yet does not physiologically modulate the opening of TJ in the cintestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for caused by infection, e.g. Clostridium difficile infection, concertainty infection, e.g. clostridium difficile infection, concertainty shigellosis, viral gastroenteritis, parasite concertainty and conjunt of the collegenous colitis, inflammatory bowel disease, diseases with colligenous colitis, inflammatory bowel disease, diseases with correction of congenital heart disease with frontan's operation, concertain disease, essimplical correction of congenital intestinal lymphangiectasia, collidated disease, without ulceration, e.g. Menetrics's disease, collides seventherity to the college of the colling activation and immune disease, collides, evidential intestinal and immune disease, colling active partylematics and immune disease, and immune disease, and immune disease, colling active partylematics and contentity to the colling active partylematics.
                                                    blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulicer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic; gastrointestinal inflammation; therapy.
                                                                                                                                                         Zonulin;
                                                                                                                                                                                                                                         05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 43; 69pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This present sequence is that of a peptide antagonist of zonul (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (ZOT) receptor, yet do physiologically modulate the opening of mammalian tight junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-205565/18
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                                                                                                                                                                                                 Peptide antagonist of zonulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        I GRVCVQPG 8
                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                         antagonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                    Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
                                                                                                                                                         zonula occludens toxin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 21; Pred. No. 3.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  얶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergies, primarily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
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antagonist of zonulin.

05-JUN-2000 Y79106

(first entry)

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Zonulin; antagonist; zonula occludens toxin receptor; blood brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antialler

antiallergic;

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RESULT
Y79106
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                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whipple's disease, diseases with conlargenous colitis, inflammatory bowel disease, diseases marked by the content of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      correction of congenital heart disease with Fontan's operation, mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which bind to a zonula occludens toxin (ZOT) receptor, y physiologically modulate the opening of mammalian tight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis,
Y79106 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphatic obstruction, e.g. congenital intestinal lymphangiectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 45; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fasano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
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                                                                                                                               1 ggvcvqpg
                                                                                                                                                                                        1 GRVCVQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               systemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            logically modulate the opening of mammalian tight junctions The peptide antagonists are based on a common motif of 20T man zonulins, which is believed to be critical for receptor.
                                                                                                                                                                                                                                           Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ebral ischemia, stroke, cerebral ede viral gastroenteritis, meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARYLAND BALTIMORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence is that of a peptide antagonist of zonul such peptides (see Y79105-29) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0127815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythematosus
                                                                                                                                                                                                                                                                    84.8%;
                                                                                                                                                                                                                                           Score 39; DB
Pred. No. 3.2e
0; Mismatches
                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                 DΒ
                                                                                                                                                                                                                                                                    2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergies,
                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antagonist of zonulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor, yet do not
                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encephalomyelitis
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RESULT
R34476
ID R3
XX
AC R6
XX
DT 3(
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding. They can be prepared by chemical synthesis or by use of crecombinant DNA techniques. The peptide antapoints are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangiactasia, correction of congenital heart disease with Fontan's operation, a mucosal diseases with beart disease with Fontan's operation.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
Encoded by Hepatitis C virus
                                                                         R34476;
                                30-JUL-1993 (first entry)
                                                                                                           R34476 standard; Protein; 470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by near recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                              mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune disee.g. systemic lupus erythematosus or food allergies, primarily
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (20T) receptor, yet do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 41; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigeliosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-205565/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotensive; immunosuppressive; antiparasitic; vasotropic; gastrointestinal inflammation; therapy.
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                                                                                                                                                                                                                                                                                         82.6%;
87.5%;
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                                                                                                                                                                                                                                                                                         Score 38; Pred. No.
clone JK4-A
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                       2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                               and immune diseases, rgies, primarily to
                                                                                                                                                                                                                                                                                                        Length 8;
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PR XX DR DR XX
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Best Local Similarity
DNA and cDNA of hepatitis C virus - useful as probes for diagnosing HCV infection
                                   WPI; 1993-130638/16.
N-PSDB; Q40435.
                                                                                                 30-MAY-1991;
                                                                                                                        30-MAY-1991;
                                                                                                                                                                       JP05068562-A.
                                                                                                                                                                                              Hepatitis C virus
                                                                                                                                                                                                                   HCV; non-A, non-B hepatitis virus; NANBHV; liver disease;
polymerase chain reaction; diagnostic method.
                                                                                                                                                                                                                                                         Encoded by
                                                                                                                                                                                                                                                                                30-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                          R34477;
                                                                                                                                                                                                                                                                                                                               R34477 standard; Protein; 470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA was prepared from HCV genomic RNA. Full-length clone JK1-B (9405 nucleotides long) and 14 shorter clones were isolated by PCR amplification, including clone JK4-A. Primer/probes derived from the sequences of these clones can be used in diagnostic assays for HCV.
                                                                     (SANW ) SANWA KAGAKU
                                                                                                                                                23-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 32-34; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA and cDNA of hepatitis C virus - useful as probes diagnosing HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q40434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See Q40425-Q40439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-130638/16.
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polymerase chain reaction; diagnostic method.
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                                                                                                                                                                                                                                                                                                                                                                                          gracaqpg
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                                                                                                                                                                                                                                                       Hepatitis C virus clone JK4-B
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                                                                                                91JP-0153736.
                                                                                                                       91JP-0153736.
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                                                                        KENKYUSHO CO
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75.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ed. No. 38;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Length 470;
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RESULT
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Best Local S
Matches 6
                                                                                                                                            Query Match
Best Local
                                                                                                                                Matches
                                                                                                                                                                                                                                           cDNA was prepared from HCV genomic RNA. Full-length clone JK1-B (9405 nuclectides long) and 14 shorter clones were isolated by PCR amplification, including clone JK4-C. Primer/probes derived from th sequences of these clones can be used in diagnostic assays for HCV. See Q40425-Q40439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA was prepared from HCV genomic RNA. Full-length clone JK1-B (9405 nucleotides long) and 14 shorter clones were isolated by PCR amplification, including clone JK4-B. Primer/probes derived from the sequences of these clones can be used in diagnostic assays for HCV. See Q40425-040439.
                                                                                                                                                                                                                                                                                                                                                                        DNA and cDNA of hepatitis C virus - useful as diagnosing HCV infection
                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                             Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q40436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain reaction;
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                                                                73
                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 gracaqpg 80
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                                                              gracaqpg
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                                                                                                                                                                                                              470 AA;
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                                                                                                                               Conservative
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75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                          Japanese.
                                                                                                                             Score 38; DB Pred. No. 38; 0; Mismatches
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                                                                                                                                         38;
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                                                                                                                                                             Length 470;
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RESULT
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Best Local
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                                                                                                                                          Peptide
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                                                                                                                                                                            05-JUN-2000
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                                                                                                                                                                                                                                         79107 standard;
                                                                                                                                                                                                                                                                                                                                          1 GRVCVQP
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                                                                                                                                                                                                                                                                                                                                                                                       6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1291 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                           1070
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                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                           Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                        80.4%;
85.7%;
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This sequence represents murine tyrosine phosphatase MPTP-delta. The CDNA sequence encoding this protein was isolated from murine brain tissue and was cloned, for expression, into the downstream region of collatathione-S-transferase sequence and expressed as a fusion protein in E. coli. MPTP-delta proteins regulate differentiation and activation of cells. This sequence can be used in the elucidation of the molecular mechanism for information transmission in cells, regulation mechanisms in the nervous system or immune system, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine phosphatase MPTP-delta; murine; brain tissue; glutathione-S-transferase; fusion protein; E. coll; differentiation; activation; information transmission; nervous system; immune system;
gastrointestinal inflammation; therapy
                                   antibacterial; cytostatic; anti-HIV; vulnerary;
hypotensive; immunosuppressive; antiparasitic; v
                                                                                                       Zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 5-11; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding tyrosine phosphatase MPTP delta - elucidation of signal transmission mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine phosphatase MPTP-delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the mechanism of carcinogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TOKS-) TOKYOTO SHINKEI KAGAKU SOGO KENKYUSHO ZH.
                                                                                                                                                                                                                                                                  antagonist of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 16;
Pred. No. 1.4e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                   antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 7; Conserv
Zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangiectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                               05-JUN-2000
                                                                                                                                                    Y79121
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                   Y79121 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 41; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-205565/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200007609-A1.
                                                                                                                                                                                                                                                                       1 grvlvqpg
                                                                                                                                                                                                                                                                                              1 GRVCVQPG 8
                                                                         antagonist of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  78.3%;
87.5%;
                                                                                                                                                                                                                                                                                                                                               Score 36; DB
Pred. No. 3.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                  DB 21;
.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                 Length 8
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05-JUN-2000

(first entry)

RESULT 12 Y79110

Y79110

standard;

Peptide;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              and human zonulins, which is believed to be critical for receptor:

Chinding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an antiinflammatory agents in the treatment of gastrointestinal inflammation, where they bind to the 20T receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, wiral gastroenteritis, parasite infestation, becterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangictasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, e.g. coeliac disease, eosiophilic gastroenterities, and immune disease, coeliac disease, eosiophilic gastroenterities, and immune disease,
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (ZOT) receptor, yet do not physiologically modulate the opening of mammalian tight junctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 46; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic;
hypotensive; immunosuppressive; antiparasitic; vasotropic;
gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYMA-) UNIV MARYLAND BALTIMORE
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                                                                                                                                                    Local Similarity es 6; Conserv
1 gglcvqpg
                                                                            1 GRVCVQPG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide antagonists are based on a common motif of 20T nan zonulins, which is believed to be critical for receptor they can be receptor to the control be continued to the control be control to the control be control to the cont
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           erythematosus
                                                                                                                                                                                   78.3%;
                                                                                                                                                                                   Score 36; I
                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                or food allergies, primarily to
                                                                                                                                                                                   DB 21;
3.2e+05;
                                                                                                                                                                                                                 Length 8;
                                                                                                                                                 Indels
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                                                                                                                                             Gaps
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RESULT
R20006
ID R20
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Best Local
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                                                                                                                                                                                                                                                                                                            mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune disce.g. systemic lupus erythematosus or food allergies, primarily
                                                                                                                                                                                                                                                                                                                                                                enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangiectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor and property. They can be prepared by chemical synthesis or by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic;
R20006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (ZOT) receptor, yet do not physiologically modulate the opening of mammalian tight junctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 42; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYMA-) UNIV
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                                                                                          grlcvqdg
                                                                                                                              GRVCVQPG
                                                                                                                                                                Similarity 6; Conser
                                                                                                                                                                                                                                                            8
                                                                                                                                                                  Conservative
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Protein; 399 AA
                                                                                                                                                                              76.18;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zonula occludens toxin receptor;
                                                                                                                                                              Score 35; DB pred. No. 3.26
1; Mismatches
                                                                                                                                                                                                 DB
                                                                                                                                                                                  2e+05;
                                                                                                                                                                                                   21;
                                                                                                                                                                                                   Length 8;
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arily to
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RESULT 14
W13574
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
""" 6; Conserv
                              06-MAR-1997.
          27-AUG-1996;
                                                                                            signal
                                                                                                        Beta-3
                                                                                                                             Mouse beta-3
                                                                                                                                                 03-JUN-1997
                                                                                                                                                                        W13574;
                                                                                                                                                                                            W13574 standard;
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                             It may be responsible for diarrhoea in some strains of cholera and the ZOT gene or fragments of it are deleted from strains of Vibrio cholerae (V.c.) to be used as vaccines. These V.c. strains fave 100% efficacy in protecting humans against subsequent infection with a strain of a similar scrotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09118979-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
                                                   WO9708316-A1
                                                                        Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 18; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-007465/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaper JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZOT; cholera; vaccine; enterotoxin; diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                    used for prodn. of vaccines against cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                              The amino acid sequence is that of the zonula occludens toxin (ZOT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Vibrio cholerae strains - fragment encoding toxin, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zonula occludens
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                                                                                                                                                                                                                                               291 grlcvqdg 298
                                                                                                                                                                                                                                                                    1 GRVCVQPG 8
                                                                                              transduction;
                                                                                                         integrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                399 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                            integrin (truncated).
                                                                                                                                                 (first entry)
           96WO-US13805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-US03812
                                                                                            bone resorption; osteoporosis;
ion; vitronectin receptor.
                                                                                                                                                                                           Protein; 720
                                                                                                                                                                                                                                                                                                     76.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ins - comprise restriction used as vaccines against of
                                                                                                                                                                                                                                                                                           Score 35; DB Pred. No. 1.1e
1; Mismatches
                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fasano A;
                                                                                                                                                                                                                                                                                                     DB 13;
1.1e+02;
                                                                                                                                                                                                                                                                                                               Length 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n endonuclease
cholera
                                                                                                                                                                                                                                                                                            Indels
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31-AUG-1995;

95US-0003020.

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RESULT 15
W13573
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel truncated mouse vitronectin integrin receptor beta-3 subunit (W13574) lacks the transmembrane and cytoplasmic domains of the full-length receptor (see also W13573) and is considered to be a soluble ligand binding integrin that is able to circulate throughout the organism and to suppress or compete with the normal signals mediated by the wild-type receptor. It can be produced in host cells utilising a novel cDNA clone (T61291). The full-length and truncated beta-3 integrin subunits can be used in assays to identify novel cpds. which inhibit the bone absorption process, esp.in osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse full length or truncated beta-3 integrin sub-unit(s) and coding sequences - useful for screening for cpds. that inhibit bone
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VCVQPG 8
||||||
612 vcvqpg 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Fig 3A-3B; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duong LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resorption
                                                                                                                                                                                                                                                                             Beta-3 integrin; bone resorption; osteoporosis; osteoclast;
signal transduction; vitronectin receptor.
                                                                                                                                                                                                                                                                                                                                                                                        W13573 standard; Protein; 787
                                                                                                                                                                                                                                                                                                                                        03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                 W13573;
                     Mouse full length or truncated beta-3 integrin sub-unit(s) and coding sequences - useful for screening for cpds. that inhibit bone resorption
                                                                                                        Duong LT,
                                                                                                                                                         31-AUG-1995;
                                                                                                                                                                                  27-AUG-1996;
                                                                                                                                                                                                         06-MAR-1997
                                                                                                                                                                                                                                WO9708316-A1
                                                                                                                                                                                                                                                                                                                   Mouse beta-3 integrin
                                                                        N-PSDB; T61290.
                                                                                 WPI; 1997-179273/16
                                                                                                                                  (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nutt EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720 AA;
                                                                                                           Nutt EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                           95US-0003020
                                                                                                                                                                                  96WO-US13805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%; Score 35; 100.0%; Pred. No.
                                                                                                            Rodan
                                                                                                             GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Claim 10; Fig 4A-4B; 30pp; English

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*8888888888
                                        The full-length mouse vitronectin integrin receptor beta-3 subunit (W13573) can be produced in host cells utilising a novel CDNA clone (T61290) isolated from a mouse osteoclast cDNA library. The beta-3 integrin, and a novel truncated beta-3 integrin (see also W13573), can be used to screen for cpds. that bind full-length or truncated beta-3 integrin, esp. for inhibiting the bone resorption process in osteoporosis, and in an improved assay for identifying potential inhibitors of human alpha-v beta-3 receptors (i.e. inhibitors of osteoclast formation).
Sequence
787 AA;
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Query Match
Best Local Similarity
Matches 6; Conser
76.1%; Score 35; DB 18; ilarity 100.0%; Pred. No. 2e+02; Conservative 0; Mismatches 0;
                                    Length 787;
        Indels
      0
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0;

QΥ 밁 3 VCVQPG 8 |||||| 612 VCVqpg 617

Search completed: June 13, 2001, 14:14:29 Job time: 370 sec

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June 13, 2001, 14:08:19 ; Search time 130.61 Seconds (without alignments) 4.209 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        198801 segs, 68722935 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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pir2:*
pir3:*
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                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

integrin beta-3 ch integrin beta-3 ch epithelial cell gl probable DNA-direc glycoprotein G - s platelet glycoprot platelet glycoprot platelet glycoprot platelet glycoprot platelet glycoprot platelet glycoprot protein-tyrosine-p protein-tyrosine-p glycerol kinase PA prote prote anthranilate synth probable glycerol DNA-directed DNA p hypothetical prote genome polyprotein probable lipoprote zona occludens tox 63K sperm flagella hypothetical prote zonula occludens t probable carbohydr glycerol kinase hypothetical hypothetical early E4 31K hypothetical Description SUMMARIES \$18032 D83228 D546892 D54689 C54689 H83196 P83196 PN0510 PN0509 PN050 T34288 T20645 04ADG2 S74537 A70793 S39621 % Query Match Length DB 447 1691 1894 505 399 399 680 680 217 593 753 778 788 788 788 788 21827 213 226 226 283 Score Result . ₽ 

Α.J.;

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RESULT D83228

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-96 <270-7 A;Residues: 1-96 <270-7 A;Cross-references: GB:AE004756; GB:AE004091; NID:99949466; PIDN:AAG06726.1; GSPDB:GN A;Experimental source: strain PAOl

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pt A;Reference number: A82950; MUID:20437337 A;Accession: D83228

prote

hypothetical protein PA3338 [imported] - Pseudomonas aeruginosa (strain PAO1) (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Spacies: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 (Spacession: D8328 (Spacession: D8328 (Spacession: D8328 (Spacession: D8328 (Spacession: Nature P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nature 406, 959-964, 2000

DNA-directed DNA p hypothetical prote hypothetical prote probable transamin hypothetical prote T48 proteln - frui alpha-1,3-mannosyl hypothetical prote glycerol kinase (E glycrol kinase (E pyruvate decarboxy conserved hypothet hypothetical prote nucleoporin - fiss probable multi-dom hypothetical prote	ALIGNMENTS  SULT 1  B032  nome polyprotein - hepatitis C virus (isolate JK4) (fragment)  Contents: core protein; envelope protein 1; nonstructural protein 2; NSI/E2 protein  Contents: core protein; envelope protein 1; nonstructural protein 2; NSI/E2 protein  Variety: isolate JK4  Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000  Accession: S18032  Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.  Dailtred to the EMBL Data Library, September 1991  Boscription: Sequence analysis of putative structural regions of Hepatitis C Virus  Reference number: S18032  Accession: S18032  A	re 38; DB 2; Length 782; cd. No. 17; Mismatches 2; Indels 0; Gaps 0;
D46642 1721405 1721405 1721405 168333 242989 A38286	- hepatitis C virus (isolat ottain; envelope protein 1; s C virus (isolat s C virus (isolat s C virus (isolat envelope protein 1; s C virus envelope protein 1; s S.; Masashi, U.; Kobayash ence analysis of putative s S18029  nomic RNA HON> EMBH:X61594  ce: isolate JK4 titis C virus genome polypr protein; core protein; envelope protein #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status predicteenvelope protein   #status	Score 38; Pred. No. 0; Mismato
попопоннонного	ss Celologo	9 9
600 161 179 417 417 417 447 508 508 570 672 672 692 692 118 2240	cotein - hepatitis C vir core protein; envelope F patitis C virus colate JK4 n-1992 #sequence_revisi S18032 Kaneko, S.; Masashi, U. the EMBL Data Library, sequence analysis of S18039 S18039 S18039 Pe: Sequence analysis of cumber: S18029 Pe: Sequence analysis of conces: EMBL:X61594 il source: isolate JK4 : hepatitis C virus ger apsid protein; core protein cot: core protein #statu duct: nonstructural productin duct: nonstructural productin	82.6%; larity 75.0%; Conservative
	oce in the proof of the proof o	rit
000000000000000000000000000000000000000	octein - oct	Similarity 6; Conser
115555555555555555	RESULT 1 518032 genome polyprotein - hepatitis C virus %:Contains: core protein; envelope prof C:Species: hepatitis C virus A:Variety: isolate JK4 C:Species: 30-Jun-1992 #sequence_revision C:Accession: 518032 R:Honda, M.; Kaneko, S.; Masashi, U.; R submitted to the EMBL Data Library, Sep A:Description: Sequence analysis of put A:Reference number: 518029 A:Reference number: 518029 A:Accession: 518032 A:Accession: 1-782 cHON> A:Residues: 1-782 cHON> A:Cross-references: EMBL:X61594 A:Cross-references: EMBL:X61594 C:Superfamily: hepatitis C virus genome C:Keywords: capsid protein: socie protein F:1-191/Product: core protein #status F:192-383/Product: envelope protein   F:384-733/Product: nonstructural protein F:734-782/Product: nonstructural protein	atch cal
01000000000000000000000000000000000000	RESULT 1 S18032 genome polypr N;Contains: c C;Species: e A;Variety: is C;Date: 30-Ju C;Date: 30-Ju C;Date: 30-Ju S;Honda, M; Submitted to A;Description A;Reference n A;Reference n C;Superfamily C;Reference n C;Reference n C;Re	Query M Best Lo Matches

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A; Gene: PA3338 C; Genetics

Gaps ö Length 96; Indels DB 2; 3; Mismatches Score 37; Pred. No. 80.4%; 62.5%; Conservative Query Match Best Local Similarity Matches 5; Conserv

1 GRVCVQPG·8 ð

1:||::|| 38 GKVCLEPG 45

probable lipoprotein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999 C:Accession: T34992 R:Ollver, K:; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A:Reference number: Z21550 A:Reference number: Z21550 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Nolecule type: DNA A:Residues: 1-447 <0LI>

A;Cross-references: EMBL:AL031182; PIDN:CAA20169.1; GSPDB:GN00070; SCOEDB:SC4A2.17c A;Experimental source: strain A3(2) C;Genetics:

A; Gene: SCOEDB:SC4A2.17c

Gaps ; 0 Score 37; DB 2; Length 447; Pred. No. 16; 1; Mismatches 0; Indels Indels 85.7%; Query Match 80.4 Best Local Similarity 85.7 Matches 6; Conservative

1 GRVCVQP 7 ||:|||| 31 GRLCVQP 37 å

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Description of the phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor NyAlternate names: MPTP delta type D

NyAlternate names: MPTP delta type D

C:Species: Mus musculus (house mouse)

C:Species: Mus musculus (house mouse)

C:Species: Nus musculus (house mouse)

C:Species: Nus musculus (house mouse)

C:Accession: D54689; Asf489

R:Mittuno, K.; Masegawa, K.; Kandagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Noi. Cell. Biol. 13, 5513-5523, 1993

A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialize A;Recession: D54689; MUID:93360986

A;Accession: D54689; MUID:93360986

A;Accession: D54689; MUID:93360986

A;Restues: preliminary

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:136537)

A;Status: preliminary

A;Mote: sequence inconsistent with nucleotide translation

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence inconsistent with nucleotide franslation

A;Note: sequence extracted from NCBI backbone (NCBIN:135522, NCBIP:136524)

A;Status: preliminary

A;Note: sequence extracted from NCBI backbone (NCBIN:135522, NCBIP:136524)

C;Superfamily: leukocyte antigen-related protein; fibronectin; phosphoric monoester hyd

C;Keywords: alternative splitcing; glycoprotein; phosphoric monoester hyd

C;Keywords: alternative splitcing; glycoprotein; phosphoric monoester hyd

E;142-95/Domain: immunoglobulin homology <i two. F;142-95/Domain: immunoglobulin nucleon antigen cytosolic domain homology <IMC)

F;114-196/Domain: leukocyte common antigen cytosolic domain homology <IMC)

s predicted \*\*status\*\* F;1333/Active site: Cys (phosphocysteine intermediate) #status predicted F;1339/Binding site: substrate phosphate (Arg) #status predicted F;1623/Active site: Cys (phosphocysteine intermediate) #status predicted F;1629/Binding site: substrate phosphate (Arg) #status predicted protein-tyrosine-phosphatase homology F;1449-1671/Domain:

Gaps ö Length 1691; Indels ä Score 37; DB 1 Pred. No. 52; 1; Mismatches Query Match 80.4 Best Local Similarity 85.7 Matches 6; Conservative

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1464 GRVCLQP 1470 1 GRVCVQP 7 ò

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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precur N;Alternate names: MTP delta type B/C
N;Alternate names: MTP delta type B/C
Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 12-Feb-1999
C;Accession: C34689; B54689
R;Mizuno, K.: Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993 R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in special
A;Reference number: A54689; MUID:93360986
A;Accession: C54689

A; Status: preliminary

A; Molecule type: mRNA A; Residues: 1.1894 <MIZ> A; Experimental source: brain; splice form B A; Note: sequence inconsistent with nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)

A; Accession: B54689

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A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-352, 'H', 354-535,'S',537-601,1002-1894 <MI2>
A; Experimental source: brain; splice form C
A; Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

Cyteywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester F145-107/Domain: immunoglobulin homology <IRMI> F1245-299/Domain: immunoglobulin homology <IRMI> F1245-299/Domain: immunoglobulin homology <IRMI> F1245-299/Domain: immunoglobulin homology <IRMI> F1278-1894/Domain: leukocyte common antigen cytosolic domain homology <IRC> F1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2> F1554/Active site: Cys (phosphocyteine intermediate) #status predicted F1826/Active site: Cys (phosphocysteine intermediate) #status predicted F1826/Active site: Cys (phosphocysteine intermediate) #status predicted F1832/Binding site: substrate phosphate (Arg) #status predicted

Gaps ö DB 2; Length 1894; 58; ö 80.4%; Score 37; DB 85.7%; Pred. No. 58; cive 1; Mismatches Conservative Query Match Best Local Similarity Matches 6; Conserv

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1 GRVCVQP 7 ò

1667 GRVCLQP 1673 qq

RESULT

н83196

"Glycerol kinase PA3582 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000
C;Accession: H83196
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

14:59:26 2001 Wed Jun 13

ö

Gaps

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integrin beta-3 chain - rat (fragment)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 0.3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C; Accession: PN0509
R; Cieutat, A.M.; Rosa, J.P.; Letourneur, F.; Poncz, M.; Rifat, S.
Biochem. Blophys. Res. Commun. 193, 771-778, 1993
A; Title: A comparative analysis of CDNA-derived sequences for rat and mouse beta-3 in A; Reference number: PN0509; MUID:93290675
A; Reference number: PN0509
A; Reference number: nucleic acid sequence not shown
A; Releas: 1-723 ccirs
C; Superfamily: integrin beta chain; laminin-type EGF-like homology
C; Superfamily: integrin beta chain; heterodimer; membrane protein
                                                                                                                                                                                                                                                                                                                                                                            C.Species: Mus musculus (house mouse).
C.Species: Mus musculus (house mouse)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C.Accession: PN0510
R.Cieutat, A.M.: Rosa, J.P.; Letourneur, F.; Poncz, M.; Rifat, S.
Blochem. Blophys. Res. Commun. 193, 771-778, 1993
A.Title: A comparative analysis of CDNA-derived sequences for rat and mouse beta-3 in A.Title: A comparative analysis of CDNA-derived sequences for rat and mouse beta-3 in A.Title: A comparative analysis of SDNA-derived sequences for rat and mouse beta-3 in A.Title: A comparative analysis of CDNA-derived sequences for rat and mouse beta-3 in A.Title: A comparative analysis of CDNA-derived sequences for rat and mouse beta-3 in A.Secession: PN0510
A.Status: nucleic acid sequence not shown
A.Nolecule type: mRNA
A.Nolecule type: mRNA
A.Nolecule type: mRNA
A.Rosidues: 1-680 <CIE>
C.Superfamily: integrin beta chain; laminin-type EGF-like homology
C.Superfamily: cil adhesion; duplication; heterodimer; membrane protein
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D37057
C. Species: Cavia porcellus (guinea pig)
C. Species: Cavia porcellus (guinea pig)
C. Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 23-Jul-1999
C. Accession: D37057
R. Sheppard, D.: Rozzo, C.: Starr, L.: Quaranta, V.: Erle, D.J.: Pytela, R.
J. Biol. Chem. 265, 11502-11507, 1990
A/Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 680;
56;
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59;
                                       Length 399
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                                    DB 2;
35;
                                                                                              1; Mismatches
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                                    Score 35;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                         integrin beta-3 chain - mouse (fragment)
                                    76.1%;
75.0%;
                                                                                              6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                               Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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291 GRLCVQDG 298
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509 VCVQPG 514
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548 VCVQPG 553
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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
ArItle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337
A;Accession: H83196
                                                                                                                                        A Status: preliminary
A Molecule type: DNA
A; Residues: 1-505 <STO>
A; Cross-references: GB:AE004779; GB:AE004091; NID:g9949735; PIDN:AAG06970.1; GSPDB:GN001
A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:AAF94615.1; GSPDB:GN001
El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Vibrio cholerae
(C; Date: 18-Nug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
(C; Date: 18-Nug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
(C; Accession: B82197
(R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Wekalaenos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Vibrio cholerae
C; Date: 10-Mar-1993 #sequence_revision.18-Nov-1994 #text_change 08-Oct-1999
C; Accession: A43864 #sequence_revision.18-Nov-1994 #text_change 08-Oct-1999
R; Baudry, B.; Fasano, A.; Ketley, J.; Kaper, J.B.
Infect. Immun. 60, 428-434, 1992
A; Title: Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.
A; Reference number: A43864; MUID:92112300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zona occludens toxin VC1458 [imported] - Vibrio cholerae (group Ol strain N16961)
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A:Note: sequence extracted from NCBI backbone (NCBIN:77488, NCBIP:77491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A MESIdues: 1-399 < HEI>
A MICROSS - Teferences: GB.AE004224; GB.AE003852; NID:99655952; A Experimental source: serogroup OI; strain N16961; blotype C Genetics: A Molecule NC1458 A Molecule NC1458 A Molecule NC1458
                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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Pred. No. 35;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
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62.5%;
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75.0%;
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                  A;Gene: glpK; PA3582
C;Superfamily: xylulokinase
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-399 <BAU>
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256 GQMCVEPG 263
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291 GRLCVQDG 298
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Gaps

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A;Status: now, oo
A;Status: not compared with conceptual translation
A;Mosteduse: 1979: mRNA
A;Easiduse: 1-778 <ROS>
R;Lanza, F.; Kieffer, N.; Phillips, D.R.; Fitzgerald, L.A.
J. Biol. Chem. 265, 18098-18103, 1990
A;Title: Characterization of the human platelet glycoprotein IIIa gene. Comparison with A;Reference number: A36085; MUID:91009291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       platelet glycoprotein IIIa beta chain (version 2) - human (fragment)
N;Alternate names: antigen CD61; integrin beta 3
C;Specias: Homo saplens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C;Accession: A60798; A36085; D32528; A36268
C;Accession: A60798; A36085; D32528; C32528; A36268
B;Rosa, J.P.; Bray, P.F.; Gayet, O.; Johnston, G.I.; Cook, R.G.; Jackson, K.W.; Shuma Blood 72, 593-600, 1988
A;Title: Cloning of glycoprotein IIIa cDNA from human erythroleukemia cells and local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1753 <21M>
A; Cross-references: GB:J05427
B; Van Kuppevelt, T.H.M.S.M.; Languino, L.R.; Gailit, J.O.; Suzuki, S.; Ruoslahti, E. Proc. Natl. Acad. Sci. U.S.A. 86, 5415-5418, 1989
A; Title: An alternative cytoplasmic domain of the integrin beta-3 subunit.
A; Reference number: A33907; MUID:89315807
A; Accession: A33907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.; Bennett, J.S.; White II, G.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Van-1991 #sequence_revision 13-Jan-1993 #text_change 20-Aug-1999
C;Accession: B35268, A39200
R;Zimrin, A.B.; Gidwitz, S.; Lord, S.; Schwartz, E.; Bennett, J.S.; White II
J;Biol. Cham. 265, B890-08955, 1990
A;Title: The genomic organization of platelet glycoprotein IIIa.
A;Reference number: A36268; WUID:90256778
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A;Residues: 17-705,'G',707-778 <LAN>
A;Cross-references: GB:M7494
R;HIraiwa, A.; Matsukage, A.; Shiku, H.; Takahashi, T.; Naito, K.; Yamada,
                                                                                                Gaps
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A; Residues: 680-753 < VAN>
A; Cross-references: GB:M25108; NID:g186502; PIDN:AAA36121.1; PID:g386833
C; Superfamily: integrin beta chain; laminin-type EGF-like homology
C; Reywords: cell adhesion; glycoprotein
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                                    DB 2;
76;
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94;
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Pred. No. 94;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                            platelet glycoprotein IIIa-II - human (fragment)
                                                                                                0; Mismatches
                                    Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: integrin beta-3' chain
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83.3%;
                                 73.9%;
75.0%;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                Conservative
                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                            248 GRRCVSPG 255
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A; Status: preliminary
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586 VCIQPG 591
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A; Residues: 1-217 <CER>
A; Residues: 1-217 <CER>
A; Cross-references: GB: U34286; NID: 91236335; PIDN: AAB01080.1; PID: 91236336
A; Cross-references: GB: U34286; NID: 91236335; PIDN: AAB01080.1; PID: 91236336
B; Cermakian, N.; Ikeda, T.M.; Cedergren, R.; Gray, M.W.
Nucleic Acids Res: 24, 648-654, 1996
A; Title: Sequences homologous to yeast mitochondrial and bacteriophage T3 and T7 RNA pollar Reference number: S66158; MUID: 96177564
A; Reference number: S66158; MUID: 96177564
A; Accession: S66150
A; Molecule type: mRNA
A; Residues: 1-20; 33-66; 130-217 <CEW>
A; Cross-references: GB: U34286
A; Cross-references: GB: U34286
A; Cross-references: GCMP: 1203
C; Superfamily: phage T7 DNA-directed RNA polymerase
C; Keywords: nucleotidyltransferase; transcription
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N.Alternate names: T3/T7-like NNA polymerase
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NyAlternate names: US4 protein homolog
C;Species: simian herpesvirus B
C;Species: simian herpesvirus B
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: S49525
R;Slonka, M.J.; BrCom, D.W.
A;Description: Complete nucleotide sequence of simian herpes B virus glycopi
A;Reference number: S49525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Pycnococcus provasolin: Frightness C;Species: Pycnococcus provasolin: C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 26-May-2000 C;Accession: S66155; S66160 R;Cernakian; N.; Ikeda, T.M.; Cedergren, R.; Gray, M.W. submitted to the EMBL Data Library, August 1995 A;Reference number: S66152 A;Accession: S66155
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A;Residues: 1-593 <SLO>
A;Cross-references: EMBL:Z46268; NID:g560495; PIDN:CAA86431.1; PID:g560496
A;Experimental source: isolate Cyno 2
C;Keywords: glycoprotein
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A; Reference number: A37057; MUID:90307659
A; Accession: D37057
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: MRNA
A; Residues: 1-92 <SHE>
A; Cross-references: GB:J05522
C; Superfamily: Integrin beta chain; laminin-type EGF-like homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 217; 31;
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Pred. No. 15;
1; Mismatches
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Pred. No. 3
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Best Local Similarity 85.7%;
Matches 6; Conservative (
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ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 5; Conserv
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82 VCIOPG 87
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A: Molecule type: protein
A: Residues: 208-224 <HI2>
A: Residues: 208-224 <HI2>
A: Residues: 208-224 <HI2>
A: Residues: 208-234 <HI2>
A: Molecule type: protein
A: Residues: 429-433 <HIP:
A: Residues: 429-433 <HIP:
J. Biol. Chem. 265, 8590-8595, 1990
J. Biol. Chem. 265, 8590-8595, 1990
A: Title: The genomic organization of platelet glycoprotein IIIa.
A: Reference number: A36268; MUID: 90256778
A: Accession: A36268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
Kresidues: 18-705,'G',707-778 <2IM>
A; Cross-references: GB:J05427
A; Note: the authors translated the codon GAT for residue 233 as Glu, GAT for residue 249
A;Title: Purification and partial amino acid sequence of human platelet membrane glycopi
A;Reference number: A90731; MUID:87101510
A;Accession: D32528
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A;Map position: 17q21.32-17q21.32
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
C;Keywords: alternative splicing; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
73.9%; Score 34; DB 2; Length 778;
Best Local Similarity 83.3%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 0; Indels
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A;Gene: GDB:ITGB3
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Search completed: June 13, 2001, 14:10:36 Job time: 137 sec

11:111 603 VCIQPG 608 3 VCVQPG 8

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GenCore version 4.5
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OM protein - protein search, using sw model

June 13, 2001, 14:08:20 ; Search time 74.44 Seconds (without alignments) 3.681 Million cell updates/sec Run on:

PCT-US01-05825A-1 46 1 GRVCVQPG 8 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			O54890 mus musculu	P05106 homo sapien	P03242 human adeno	. Q9t091 arabidopsis		Q9x1e4 thermotoga		O69664 mycobacteri	_		Q14181 homo sapien	mus m		homo	cerco		σ.	024495 arabidopsis	6	₩.	Ś	P47284 mycoplasma	3287	O15169 homo sapien	_	O26669 methanobact	7	572	2	0932	P22427 equine infe .
SUMMARIES	ΩI	GLPK_PSEAE	ZOT_VIBCH	ITB3_MOUSE	ITB3_HUMAN	EXXK_ADE02	VP26_ARATH	SP63_STRPU	GLK2_THEMA	TRPE_SYNY3	GLPK_MYCTU	DLL3_RAT	DLL3_MOUSE	DPO2_HUMAN	DPO2_MOUSE	DLL3_HUMAN	P73_HUMAN	P73_CERAE	PG20_AGKBL	Y281_METJA	GL2M_ARATH	SUR6_MOUSE	YFDZ_ECOLI	GNT1_RABIT	GLPK_MYCGE	DCPY_NEUCR	AXN1_HUMAN	AXN1_MOUSE	HTPX_METTH	EF1G_TRYCR	GNT1_HUMAN	GNT1_MOUSE	GNT1_RAT	ENV_EIAV1
	Length DB	505 1	399 1				.298 1										636 1							447 1										859 1
o#	Query	78.3		ė.		71.7			71.7	71.7	71.7	71.7	71.7	71.7		71.7	Н	Н	σ	9	9.69	σ	9.69	9.69	σ,	σ.	σ	σ	ζ.	7	67.4	67.4		67.4
	Score	36	35	35	34	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	31
	Result No.		7	e	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	52	26	27	28	29	30	31	32	33

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ENV_EIAV2 ENV_EIAV3 ENV_EIAV9 ENV_EIAV6 ENV_EIAVW ENV_EIAVW CASALUMAN YLBB_CAEEL ATC2_HUMAN ATC2_PIG ATC2_ROSE
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## ALIGNMENTS

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MEDLINE-91271365; Pubmed-2052603;
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ITB3_MOUSE
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MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID-666;
                                                                                                                                                                                                                                                                                                                                                                                             Baudry B., Fasano A., Ketley J., Kaper J.B.;
"Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene
cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35:205-210(1999).
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                                                                                                                Length 505;
                                                                                                                                       Indels
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STRAIN-EL TOR 86015 / SEROTYPE 01;
Kan B., Liu Y.Q., Q1 G.M., Gao S.Y.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
PS00445; FGGY_KINASES_2; 1.
PS00933; FGGY_KINASES_1; 1.
metabolism; Transferase; Kinase; ATP-binding.
158 170 ATP (PROBABLE).
75 75 H -> R (IN REF. 1).
104 104 A -> V (IN REF. 1).
109 109 C -> R (IN REF. 1).
505 AA; 55966 MW; CC63A9ARF8ABGEF752 CRC64;
                                                                                                                                                                                                                                     201_VIBCH STANDARD; PRT; 399 AA. P38442; 09L706; 09R3V6; 01-0CT-1994 (Rel. 30, Created) 1-CCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 20NA OCCLUDENS TOXIN (ZONULAR OCCLUDENS TOXIN)
                                                                                                                1;
                                                                                                               Score 36; DB 1
Pred. No. 10;
3; Mismatches
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MEDLINE-92112300; PubMed-1730472;
                                                                                                                                      3;
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                                                                                                               Query Match 78.3%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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256 GQMCVEPG 263
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CHARACTERIZATION.
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Vibrio cholerae.
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                       Glycerol
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   PROSITE;
               PROSITE;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Fasano A., Baudry B., Pumplin D.W., Wasserman S.S., Tall B.D., Ketley J.M., Kaper J.B.;
"Vibrio cholerae produces a second enterotoxin, which affects intestinal tight junctions.";
Proc. Natl. Acad. Sci. U.S.A. 88:5242-5246(1991).
-I- FUNCTION: INCREASES THE PERMEABILITY OF THE SMALL INTESTINE MUCOSA BY AFFECTING THE STRUCTURE OF INTERCELLULAR TIGHT JUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PLATELET MEMBRANE GLYCOPROTEIN IIIA PRECURSOR (GPIIIA) (INTEGRIN BETA-3) (CD61).
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V -> A (IN STRAINS 569B AND 86015).
V -> A (IN STRAINS 569B).
V -> A (IN STRAIN 569B).
V -> A (IN STRAIN 860B).
K -> K (IN STRAIN 86015).
K -> R (IN STRAIN 86015).
K -> R (IN STRAIN 86015).
IKTENDKKGLNSIF -> VKKEKEESIIKSFL (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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3C7424B758176774 CRC64;
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1; Mismatches
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EMBL, AF123049, AAD5654.1; --
EMBL, AF220606; AAF25947.1; --
EMBL, AE004224; AAF94615.1; --
ITGR, VC1458; --
Enterotoxin; Toxin.
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75.0%;
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291 GRLCVQDG 298
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Blood 83:668-676(1994).
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612 VCVQPG 617
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    CD61).
    TGB3 OR GP3A.

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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                        PLATELET MEMBRANE GLYCOPROTEIN IIIA,
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PRINTS; PR01166; INTEGRINB.
PROSITE; PS000243; INTEGRIN_BETA; 3.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat;
                     -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
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CYSTEINE-RICH REPEATS
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679
787 AA;
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ITB3_HUMAN STANDARD, PRT; 788 AA.
P05106; Q13413; Q16499;
113-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PLATELET MEMBRANE GLYCOPROTEIN IIIA PRECURSOR (GPIIIA) (INTEGRIN BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Villa-Garcia M., Li L., Riely G., Bray P.F.;
"Isolation and characterization of a TATA-less promoter for the human
                                                                                                                                                                                                                          | I.j. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-87165991; PubMed-3494014; Fitzgerald L.A., Steiner B., Rall S.C. Jr., Lo S., Phillips D.R.; Fitzgerald L.A., Steiner B., Rall S.C. Jr., Lo S., Phillips D.R.; "Protein sequence of endothelial glycoprotein IIIa derived from a cDNA clone. Identity with platelet glycoprotein IIIa and similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The gene organization of the human beta 7 subunit, the common beta subunit of the leukocyte integrins HML-1 and LPAM-1.";
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                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of platelet glycoprotein IIIa. A common subunit for different membrane receptors.";
J. Clin. Invest. 81:1470-1475(1988).
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Lanza F., Kieffer N., Phillips D.R., Fitzgerald L.A.;
"Characterization of the human platelet glycoprotein IIIa gene.
Comparison with the fibronectin receptor beta-subunit gene.";
J. Biol. Chem. 265:18098-18103(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-88213696; PubMed-2452834;
Zimrin A.B., Elsman R., Vilaire G., Schwartz E., Bennett J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90265363; PubMed-2345548; Frachet P., Uzan G., Thevenon D., Denarler E., Prandini M.H., Marguerie G.; GPIID and GPIIIa amino acid sequences deduced from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-20256778; PubMed-2341395;

Zinrin A.B., Gidwitz S., Lord S., Schwärtz E., Bennett J.S.

White G.C. II, Poncz M.;
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76.1%; Score 35; DB 1; Length 787; 100.0%; Pred. No. 24;

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Query Match Best Local Similarity Matches 6; Conserv

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                                                                                      Hiraiwa A., Matsukage A., Shiku H., Takahashi T., Naito K., Yamada K., "Purification and partial amino acid sequence of human platelet membrane glycoproteins IIb and IIIa.";
Blood 69:560-564(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A point mutation leads to an unpaired cysteine residue and a molecular weight polymorphism of a functional platelet beta 3 integrin subunit. The Sra alloantigen system of GPIIIa.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "An amino acid polymorphism within the RGD binding domain of platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuijpers R.W.A.M., Simsek S., Faber N.M., Goldschmeding R., van Wermerkerken R.K.V., von Dem Borne A.E.G.K.;
"Single point mutation in human glycoprotein IIIa is associated with a new platelet-specific alloantigen (Mo) involved in neonatal alloimmune thrombocytopenia.";
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89214713; PubMed-2565345; Newman P.J., Derbes R.S., Aster R.H.; The human platelet alloantigens, PlA1 and PlA2, are associated with a leucine33/proline33 amino acid polymorphism in membrane glycoprotein IIIa, and are distinguishable by DNA typing."; J. Clin. Invest. 83:1778-1781(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94060373; PubMed-7694683;
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"Amino acid 489 is encoded by a mutational 'hot spot' on the beta 3
integrin chain: the CA/TU human platelet alloantigen system.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane glycoprotein IIIa is responsible for the formation of the Pena/Penb alloantigen system."; J. Clin. Invest. 90:2038-2043(1992).
                                                                                                                                                                                                                                                      Calvete J.J., Henschen A., Gonzalez-Rodriguez J.;
Assignment of disulphide bonds in human platelet GPIIIa. A
disulphide pattern for the beta-subunits of the integrin family.";
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Loftus J.C., O'Toole T.E., Plow E.F., Glass A., Frelinger A.L.
Ginsberg M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A beta 3 integrin mutation abolishes ligand binding and alters divalent cation-dependent conformation."; Science 249:915-918(1990).
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Newman P.J.;
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Bajt M.L., Ginsberg M.H., Frelinger A.L. III, Berndt M.C.,
Loftus J.C.;
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BEDLINE-94179229; PubMed-8132570;
Santoso S., Kalb R., Kroll H., Walka M., Kiefel V.,
Mueller-Eckhardt C., Newman P.J.;
                                                                                                                                                                                                          PARTIAL SEQUENCE, AND DISULFIDE BONDS.
                                                                     MEDLINE-87101510; PubMed-3801670;
                                                                                                                                                                                                                                     MEDLINE-91158732; PubMed-2001252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT MO-1.
MEDLINE-93112977; PubMed-8093349;
Immunol. 4:1031-1040(1992).
                                             SEQUENCE OF 218-234 AND 439-443
                                                                                                                                                                                                                                                                                                                                                                       VARIANT HPA-1 (PL(A))
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"Ser-752-->Pro mutation in the cytoplasmic domain of integrin beta 3 subunit and defective activation of platelet integrin alpha IIb beta 3 (glycoprotein IIb-IIIa) in a variant of Glanzmann thrombasthenia.";

Proc. Natl. Acad. Sci. U.S.A. 89:10169-10173(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLYMORPHISM: POSITION 433 IS ASSOCIATED WITH PLATELET-SPECIFIC ALLOANTIGEN MO. MO(-) HAS PRO-433 AND MO(+) HAS ALA-433. MO(+) IS INVOLVED IN NATP.
                            Lanza F., Stierle A., Fournier D., Morales M., Andre G., Nurden A.T., Cazenave J.-P.,
"A new variant of Glanzmann's thrombasthenia (Strasbourg I).
Platelets with functionally defective glycoprotein IIb-IIIa complexes and a glycoprotein IIIa 214Arg-->214Trp mutation.";
J. Clin. Invest. 89:1995-2004(1992).
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-i- POLYMORPHISM: POSITION 169 IS ASSOCIATED WITH PLATELET-SPECIFIC ALLOANTIGEN HPA-4 (PEN OR YUK). HPA-4/PEN(A)/YUK(A) HAS ARC-169 AND HPA-4B/PEN(B)/YUK(B) HAS GLW-169. HPA-4B IS INVOLVED IN NEONATAL ALLOIMMUNE THROMBOCYTOPENIA (NATP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- POLYMORPHISM: POSITION 515 IS ASSOCIATED WITH PLATELET-SPECIFIC ALLOANTIGEN CA (TU). CA(-)/TU(-) HAS ARG-515 AND CA(1)/TU(+) HAS GLN-515. CA(+) IS INVOLVED IN NATP.

-!- DISEASE: DEFECTS IN ITABA ARE ONE THE CAUSE OF GLANZMANN THROMBASTHENIA (GTA). AN AUTOSOWAL RECESSIVE DISORDER WHICH IS THE MOST COMMON INHERITED DISEASE OF PLATELETS. GTA IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- ALTERNATUVE PRODUCTS: THE DIFFERENT FORMS OF BETA-3 SUBUNIT MAY
ARISE BY ALTERNATIVE SELICING OF PRIMARY MRNA TRANSCRIPTS.
-!- PIM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-3 IS EITHER ASSOCIATED WITH ALPHA-IIB (GPIIB) OR WITH ALPHA-V (VITRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Inherited diseases of platelet glycoproteins: considerations for rapid molecular characterization.";
Thromb. Haemost. 72:492-502(1994).
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Pred. No. 38;
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MEDLINE-95184171; PubMed-7878622;
MEDLINE=92291320; PubMed=1602006;
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83.3%;
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Best Local S
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MEDLINE-20083488; PubMed-10617198;
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                                                                                                                                                                                                                                                                 EARLY 31 KDA PROTEIN.
EARLY 28 KDA PROTEIN.
EARLY 14 KDA PROTEIN 2 + C-TER VRQASNY.
SECOND PART OF EARLY PROTEIN 17K.
SECOND PART OF EARLY PROTEIN 17K.
SECOND PART OF EARLY PROTEIN 20K.
SECOND PART OF EARLY PROTEIN 24K.
SECOND PART OF EARLY PROTEIN 24K.
                                                                                                           Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                    Viruses; dsDNA virūses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10515;
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26382A77A65C14DB CRC64;
                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CT-1996 (Rel. 34, Last annotation update)
PROBABLE EARLY E4 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
V01-0CT-2000 (Rel. 40, Last annotation update)
AT4G27690 OR T29A15.180
       283 AA.
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                                                                                                                                                                                                                                                                         EMBL; J01917; -; NOT_ANNOTATED_CDS.
PIR; A03808; Q4ADG2.
       PRT;
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Best Local Similarity 71.4'
Matches 5; Conservative
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      STANDARD;
                                                              Human adenovirus type 2.
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                                                                                                    SEQUENCE FROM N.A.
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223
223
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52 RVCIPPG 58
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CHAIN
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Q9T091;
      EXXK_ADE02
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RAM MEDINE-20063489; PubRed-1001/199; Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., RA MEDINE-20063489; PubRed-1001/199; Mayer K.F.X., Schueller C., Wambutt R., Bobh T., Duesterboeft A., Statekema W., Entain R., Entain R., Duesterboeft A., Statekema W., Entain R., Entain R., Machen B., Machen R., Mueller M., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Raichert B., Portetelle D., Perez-Alonso M., Boutry M., Schmidthein I., Raichert B., Portetelle D., Perez-Alonso M., Boutry M., Schmidthein I., Raichert B., Enderbert B., Schmidthein I., Annachen S.-A., McCullagh B., Bllham L., Robben J., Rart R., Defoor E., Ra Meltzeneger T., John E., Tamperger D., Hilbort H., Berlun M., Breach M., Wellyes W., Mayers M., Bancherger U., Hilbort H., Defoor E., Ra Menteneger T., Dethe G., Ramperger U., Hilbort H., Defoor E., Ra Menteneger T., Dethe G., Ramperger U., Hilbort H., Defoor E., Ra Menteneger T., Dethe G., Ramperger U., Hilbort H., Defoor E., Ra Mooijman P., Klein Lankhorst R., Yoan Gen Dele H., De Reyser A., Buysshaert C., Gellen J., Villarroel R., Poetler P., Ray and Monisqu M., Rogers J., Cronin A., Lyne M., Lannard N., McLay K., Defoor B., Bortes S., Cronin A., Lyne M., Lannard N., McLay K., Borkova D., Bloecker J., Schmafe M., Grimm M., Lochart T.-H., Doos S., de Haan M., Marse A., Schmidt W., Lecharry A., Abbourg S., Romabl S., Hiller R., Schmidt W., Lecharry A., Parandi E., Schmath S., Schmidt W., Lecharry A., Parandi S., Farnas P., Rannan S., Schmidt W., Lecharry A., Parandi S., Rajinan D., Haase D., Lemcke K., Meres H. W., Stocker S., Schmidt W., Eccharry A., Bargues M., Paranda D., Haase D., Lemcke K., Meres H. W., Stocker S., Schmidt W., Eccharry A., Stocker S., Schmidt W., Eccharry A., Stocker S., Schmidt W., Berez P., Cordes M., Paranda B., Stocker S., Schold L., Schwer S., Schold W., Bargues M., Paranda B., Schwelt D., Scheck P., Coord M., Marsey B., Schwelt D., Schwelt D
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NON_TER 1 1
SEQUENCE 298 AA; 34462 MW; 576AB065C2052DC0 CRC64;
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-!- SIMILARITY: BELONGS TO THE VPS26 FAMILY.
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Conservative
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Matches 4; Conserv
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48 GKVCIEP 54
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GRVCVOP 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEG-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
                                              SP63_STRPU STANDARD; PRT; 470 AA.
007929; P98117;
001-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
03 KDA SPERM FAGELELAR MEMBRANE PROFEIT PRECURSOR.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Echinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
63 KDA SPERM FLAGELLAR MEMBRANE PROTEIN.
REMOVED IN MATURE FORM (POTENTIAL).
EGF-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-92286182; PubMed-8509450;
Mendoza L.M., Nishioka D., Vacquier V.D.;
"A GPI-anchored sea urchin sperm membrane protein containing EGF
domains is related to uhman uromodulin.";
J. Cell Biol. 121:1291-1297(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO1180; SEA; 1.
PROSITE; PSO1186; ESF_2; 2.
PROSITE; PSO1186; ESF_2; 2.
PROSITE; PSO1187; ESF_CA; 1.
Repeat; ESF_11ke domain; Signal; Membrane; Sperm; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4D421BC147D0D1D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: SPERM.
-1- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
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Interpro; IPR000561; ...
Interpro; IPR001881; ...
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470 AA;
                                                                                                                                                                                                                                                                                          Strongylocentrotus
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein.
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RESULT 7
SP63_STRPU
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                                                                                                                                                                                                                                                 STRAIN-WSB8 / DSM 3109;
STRAIN-WSB8 / DSM 3109;
MEDLINE-99287316; Dubmed-10360571;
NELSON K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Katchum K.A.,
Horonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
412-CEROL KINASE 2 (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE 2)
(GLYCEROKINASE 2) (GK 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALVTIC ACTIVITY: ATP + GLYCEROL - ADP + GLYCEROL 3-PHOSPHATE.
-!- PATHWAY: RATE-LIMITING STEP IN GLYCEROL UTILIZATION.
-!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
GLYCEROKINASE / XYLUKKINASE FAMILY.
-!- CAUTION: A STOP CODON IN POSITION 483 WAS TRANSLATED AS TRP TO RESTORE THE SIMILARITY WITH THE C-TERMINAL REGION OF OTHERS GLPK HOMOLOGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (PROBABLE).
7FA72A4CBD29E701 CRC64;
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                                    496 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001795; AAD36500.1; ALT_SEQ.
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62.58;
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                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
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Best Local Similarity
Matches 5; Conserv
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P20170; P20168;
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                                  GLK2_THEMA
Q9X1E4;
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RESULT 8
GLK2_THEMA
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Gaps

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71.7%; Score 33; DB 1; Length 470; 71.4%; Pred. No. 37; ive 1; Mismatches 1; Indels

Conservative

Best Local Similarity Matches 5; Conserv

Query Match

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Harris

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                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ATP + GLYCEROL - ADP + GLYCEROL 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Ejglmeder K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oldrer K., Csborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton J., Squares R., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pocippering the biology of mycobacterium tuberculosis from the complete genome sequence.
                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)
GLYCEROKINASE) (GK).
GLPR OR RV3696C OR MTV025.044C.
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DELTA-LIKE PROTEIN 3 PRECURSOR (DROSOPHILA DELTA HOMOLOG 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: RATE-LIMITING STEP IN GLYCEROL UTILIZATION.
-i- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv3696c; -.
InterPro; IPR000577; -.
Pfam; PF00370; FGGY; 1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
PROSITE; PS00933; FGGY_KINASES_1; 1.
Glycerol metabolism; Transferase; Kinase; ATP-binding.
NP_BIND 165 177 ATP (PROBABLE).
SEQUENCE 517 AA; 55859 MW; 7E3F30DCF2A1EG1R CPCFA1
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ed. No. 40;
Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; PubMed-9634230;
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62.58;
                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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Best Local Similarity
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268 GQVCLAPG 275
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
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088671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                 MEDLINE-97061201; PubMed-8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Majalma N., Hirosawa M., Suguira M., Sasamoto S., Kimura T., Hasouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S.; Shimpo S., Eakeuchi C., Wada T., Watanabe A., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89034300; PubMed-3141423;
Really P., Hulmes J.D., Pan Y.C.E., Nelson N.;
"Molecular cloning and sequencing of the psaD gene encoding subunit
II of photosystem I from the cyanobacterium, Synechocystis sp. PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
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   30-MAY-2000 (Rel. 35, Last sequence update)
PROBABLE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
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SEQUENCE 508 AA; 57147 MW; A3308E9A7B8A1FC1 CRC64;
                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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100.0%; Pred. No. 40;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J04195; AAA88626.1; ALT_FRAME.
J04195; AAA88627.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 1-408 FROM N.A.
STRONG OF 1-408 FROM N.A.
STRONG OF 14023;
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Created)
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PIR; B32124; B32124
PIR; C32124; C32124
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Best Local Similarity
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Gaps

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Length 517; Indels

EMBL;

Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

517 AA

PRT;

STANDARD;

GLPK\_MYCTU ID GLPK\_MYCTU RESULT 10

Matches

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RVCLKPG
                                      RESULT 12
DLL3_MOUSE
                                                                                                                                                          DLL3.
                                               BOULTET J. Greenfield A., Welnmaster G.;

"Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";

"Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";

"Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

"I SUBMITTED (AUG-1998) to the EMBL/GenBank/DDBJ databases.

"I SUBMITTED (AUG-1998) to the EMBL/GenBank/DDBJ databases.

"I RE FORMATION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERT THE FORMATION OF THE BOUNDARIES DURING SEGMENTATION OF THE PARAXIAL MESODERM (BY SIMILARITY).

"I SUBMITT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR (BY SIMILARITY).

"I SUBMITTY: LAD BLIA-SERRATE-LAG2 (DSL) DOMAIN IS REQUIRED FOR BINDING TO THE NOTCH RECEPTOR (BY SIMILARITY).

"I SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

"I SIMILARITY: BELONGS TO THE DELTA/SERRATE/JAGGED FAMILY.
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561; ...
InterPro; IPR000742; ...
InterPro; IPR001438; ...
Pfam; PF00008; EGF_1; 6.
PROSITE; PS01186; EGF_2; 5.
SIgnal; EGF_1ke domain; Repeat; Transmembrane; Developmental protein; Differentiation.
 Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
DELTA-LIKE PROTEIN 3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A17B3BF9B95EC17F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
DELTA-SERRATE-LAG2.
EGF-LIKE 1.
EGF-LIKE 2.
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EGE-LIKE 4.
EGE-LIKE 5.
EGE-LIKE 6.
POLY-ALA.
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300
311
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589 AA;
                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00740; 11XA
                                     SEQUENCE FROM N.A.
             NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
"Specific expression of a divergent type of Delta in a set of earliest
generated neurons including the prospective supplate neurons.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNGTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERT
NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN
THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/SVJ;
MEDLINE=98324780; PubMed=9662403;
MEDLINE=98324780; PubMed=9662403;
Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,
Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;
"The mouse puddy mutafation disrupts Delta homologue Dl13 and initiation of early somite boundaries.";
Nat. Genet. 19:274-278(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND PARAXIAL MESODERM DURING EMBRYOGENESIS.

-!-DOMAIN: THE DELTA-SERRATE-LAG2 (DSL) DOMAIN IS REQUIRED FOR BINDING TO THE NOTCH RECEPTOR.

-!-DISEASE: A TRUNCATING MUTATION IN DLL3 IS THE CAUSE OF THE PUDGY (PU) PHENOTYPE. PUDCY MICE EXHIBIT PATTERNING DEFECTS AT THE EARLIEST STAGES OF SOMITOGENESIS. ADULT PUDGY MICE PRESENT SEVERE VERTEBRAL AND RIB DEFORMITIES.
DLL3_MOUSE STANDARD;
088116; 090W27; 035675; 090WL9;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
DELTA-LIKE PROTEIN 3 PRECURSOR (DROSOPHILA DELTA HOMOLOG 3) (M-DELTA-
                                                                                                                                                                                                                                                                                                                                                        Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.; "Mouse Dllia a novel divergent Delta gene which may complement the function of other Delta homologues during early pattern formation in the mouse embryo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARAXIAL MESODERM.
SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
-:- ALTERNATIVE PRODUCTS: 2 ISOPORMS; 1 AND 2 (SHOWN HERE); ARE
PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE NEUROECTODERM
                                                                                                                                                                                                                                                                                                                                              Beddington R.S.P.;
                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE DELTA/SERRATE/JAGGED FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF068865; AAC40170.1; -.
EMBL; AF068865; AAC40169.1; -.
EMBL; X11895; CAA72637.1; -.
                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6 X DBA; TISSUE-Embryo;
MEDLINE-97417575; Pubmed-9272948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 124:3065-3076(1997).
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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Gaps

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0; Indels

Mismatches

Best Local Similarity 71.4 Matches 5; Conservative

Query Match

RVCVQPG 8

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71.7%; Score 33; DB 1; Length 589; 71.4%; Pred. No. 45;

DOMAIN DOMAIN

DOMAIN

DOMAIN

DOMAIN

DOMAIN

SIGNAL

CHAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nashewer H.-P., Moore A., Wahl A.F., Wang T.S.-F.;
"Cell cycle-dependent phosphorylation of human DNA polymerase alpha.";
J. Biol. Chem. 266:7893-7903(1991).
-!- EUNCTION: MAY PLAY AN ESSENTIAL ROLE AT THE EARLY STAGE OF
CHROMOSOMAL DNA REPLICATION BY COUPLING THE POLYMERASE
ALPHA/PRIMASE COMPLEX TO THE CELLULAR REPLICATION MACHINERY (BY
                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: THE N-TERMINAL 240 AMINO ACIDS ARE SUFFICIENT TO MEDIATE COMPLEX FORMATION.
PTM: PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER, IN G2/M
                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE ALPHA SUBUNIT B FAMILY.
                                                                                                                                                                                                                     (SUBUNITS A, B, C AND D), WHICH IS ASSEMBLED THROUGHOUT THE CELL CYCLE. THE LARGEST SUBUNIT (SUBUNIT A) HAS DNA POLYMERASE ACTIVITY, THE TWO SMALLEST SUBUNITS (SUBUNITS C AND D) HAVE DNA PRIMASE ACTIVITY. SUBUNIT B BINDS TO SUBUNIT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase alpha-primase complex and their gene expression during cell proliferation and the cell cycle.";
J. Biol. Chem. 268:8111-8122(1993).
-i- FUNCTION: MAY PLAY DAN ESSENTIAL ROLE AT THE EARLY STAGE OF CHROMOSOMAL DNA REPLICATION BY COUPLING THE POLYMERASE ALPHA/PRIMASE COMPLEX TO THE CELLULAR REPLICATION MACHINERY (BY
                                                                                                                                                                                                       SUBUNIT: DNA POLYMERASE ALPHA-PRIMASE IS A FOUR SUBUNIT ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 84-102; 269-285 AND 394-403 MEDLINE-93216788; Pubmed-8463324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA POLYMERASE ALPHA 70 KDA SUBUNIT (DNA POLYMERASE SUBUNIT B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyazawa H., Izumi M., Tada S., Takada R., Masutani M., Ui M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO/SER/THR-RICH (HYDROPHILIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 598;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER.
F2ED8D6BDF4751A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA replication; Nuclear protein; Phosphorylation. DOMAIN 101 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                    PHOSPHORYLATION.
MEDLINE-91210318; Pubmed-1902230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.78;
75.08;
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 EMBO J. 12:4555-4566(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 AA;
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P33611;
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                            InterPro; IPR00056; -.
InterPro; IPR000742; -.
InterPro; IPR000742; -.
InterPro; IPR0001438; -.
Pfam; PF000008; EGF; 6.
PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00126; EGF_1; 6.
PROSITE; PS01186; EGF_2; 6.
MGD; MGI:1096877; D113.
Signal; EGF-1ike domain; Repeat; Transmembrane; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE-940838939; PubMed-8223465;
COllins K.L., Russo A.A.R., Tseng B.Y., Kelly T.J.;
"The role of the 70 KDa subunit of human DNA polymerase alpha in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 39, Last annotation update)
30 BNA POLYMERASE ALPHA 70 KDA SUBUNIT (DNA POLYMERASE SUBUNIT POLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLIQVLF -> A (IN ISOFORM 1).
-> K (IN REF. 3).
-> A (IN REF. 1).
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DELTA-LIKE PROTEIN 3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
DELTA-SERRATE-LAG2.
EGF-LIKE 1.
EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB Pred. No. 46; 2; Mismatches
                                                                                                                                                                                                       Differentiation; Alternative splicing.
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ilarity 71.4%;
Conservative
EMBL; AB013440; BAA33716.1;
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Best Local Similarity
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59 RVCLKPG 65
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Q14181;
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TRANSMEM
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RESULT 13 DPO2\_HUMAN

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Matches

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                           Repeat; Transmembrane; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
DELTA-SERRATE-LAG2.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                     DELTA-LIKE PROTEIN 3.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                              EMBL; AF241373; AAF62542.1; -
EMBL; AF241367; AAF62542.1; JOINED.
EMBL; AF241368; AAF62542.1; JOINED.
EMBL; AF241370; AAF62542.1; JOINED.
EMBL; AF241371; AAF62542.1; JOINED.
EMBL; AF241371; AAF62542.1; JOINED.
EMBL; AF241371; AAF62542.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 13, 2001, 14:21:39
Job time: 799 sec
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; 6.
SYROSITE; PS01186; EGF_2; 6.
Signal; EGF-11ke domain; Repeat; T.
Differentiation; Disease mutation.
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71.48;
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Best Local Similarity
Matches 5; Conserv
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TRANSMEM
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                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nat. Genet. 24:438-441(2000).

-I- FUNCTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERT NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE
             -1- SUBUNIT: DNA POLYMERASE ALPHA-PRIMASE IS A FOUR SUBUNIT ENZYME (SUBUNITS A, B., C AND D), WHICH IS ASSEMBLED THROUGHOUT THE CELL CYCLE. THE LARGEST SUBUNIT (SUBUNIT A) HAS DNA POLYMERASE ACTIVITY, THE TWO SMALLEST SUBUNITS (SUBUNITS C AND D) HAVE DNA PRIMASE ACTIVITY, SUBUNIT B BINDS TO SUBUNIT A. - SUBCELLULAR LOCATION: NUCLEAR. - - FURL PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER, IN G2/M PHASE (BY SIMILARITY). - - SIMILARITY: BELONGS TO THE DNA POLYMERASE ALPHA SUBUNIT B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARAXIAL MESODERM (BY SIMILARITY).
SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
DOMAIN: THE DELTA-SERRATE-LAG2 (DSL) DOMAIN IS REQUIRED FOR
BINDING TO THE NOTCH RECEPTOR.
DISBASE: DEFECTS IN DLL3 ARE A CAUSE OF AUTOSOMAL RECESSIVE
SPONDYLOCOSTAL DYSOSTOSIS (SD). IT IS CHARACTERIZED BY MULTIPLE
HEMIVERTEBRARE, RIB FUSIONS AND DELETIONS WITH A NON-PROGRESSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bustrycha: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                     PRO/SER/THR-RICH (HYDROPHILIC). 79F94BE6EF33FEBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
DELTA-LIKE PROTEIN 3 PRECURSOR (DROSOPHILA DELTA HOMOLOG 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 6 ECF-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE DELTA/SERRATE/JAGGED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.7%; Score 33; DB 1; Length 600; 75.0%; Pred. No. 46; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                   DNA replication; Nuclear protein; Phosphorylation. DOMAIN 101 107 POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618 AA
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MEDLINE-20206573; PubMed-10742114;
                                                                                                                                                                                                                                                                                                                                                                                                    66267 MW;
                                                                                                                                                                                                                                                                                                      EMBL; D13546; BAA02746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                   MGD; MGI:99690; Pola2.
                                                                                                                                                                                                                                                                                                                     PIR; B46642; B46642
                                                                                                                                                                                                                                                                                                                                                                                                  600 AA;
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Best Local Similarity
Matches 6; Conserv
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   SIMILARITY)
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Q9NYJ7;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                      Gaps
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                                              Length 618;
                                                                    0; Indels
/FTId-vàr_009952.
58A9BC0A7DEADIA0 CRC64;
                                              Score 33; DB 1;
Pred. No. 47;
2; Mismatches
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OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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Ogtun5 sus scrofa
09tun5 oryctolagus
020535 caenorhabdi
086515 mus musculu
044899 caenorhabdi
05487 caenorhabdi
094452 drosophila
09461 homo sapien
09t01 arabidopsis
04001 arabidopsis
041637 caenorhabdi
01466 homo sapien
09vuf0 mus musculu
09vuf0 mus musculu
                                                                                                                                     O9tsq9 cercopithec O35675 mus musculu O9qw12 mus musculu O9qw19 mus musculu O88671 rattus norv
                                                                                                                                                                                 Q9jjpl mus musculu
O88516 mus musculu
                                                                                                                                                                                                 069514 mycobacteri
09nyj7 homo sapien
09jjp2 mus muscul
                                                                                                                                                                                                         homo sapien
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
         09tun7
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Leonard S., Graves T., Strowmatt C.;
"The sequence of Homo sapiens PAC clone DJ0751H13.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.H.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
WUGSC:H_DJ0751H13.1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                     PRT; 4123 AA
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                                                                                                                            09WUJ0
09TSQ9
035675
09QWZ7
09QWL9
                                                                  09W452
09UHF1
09VV62
09T091
09M8J4
044637
                                                                                                                                                                                09JJP1
088516
                                                                                                                                                                                                         Q9NYJ7
Q9JJP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00057; Idl_recept_a; 11.
PF00090; tsp_1; 14.
PF00094; vwd; 5.
                        AC004877; AAC36301.1;
P01130; 1AJJ.
                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR002465;
INTERPRO; IPR002919;
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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INTERPRO; IPR002
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Submitted (S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
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 INTERPRO;
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075851;
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                                                                                                                                                                                                                                                                   RESULT
075851
099w16 rattus sp.
087588 rhizobium 1
040295 pycnococcus
059545 morganella
09uxi3 sulfolobus
032591 mazzaella 1
087093 simian herp
015495 homo saplen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    086673 streptomyce
Q64487 mus musculu
Q9xN8 Oryza sativ
Q918f5 vibrio mimi
Q91746 vibrio chol
Q91746 vibrio chol
Q9475 mus sp. bet
P79977 moorella th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    075851 homo sapien
Q68952 hepatitis c
                                                                  (without alignments)
4.152 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                        June 13, 2001, 14:08:20 ; Search time 225.85 Seconds
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                     374700 seqs, 117207915 residues
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Maximum Match 100%
Ljsting first 45 summaries
                                        - protein search, using sw model
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06852
086673
064487
09XHV8
09XHV8
09LF5
09W05
09W05
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09W15
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Q9UXI3
Q32591
Q87093
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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46
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sp_bacteria:*
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Match Length DB
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sp_mhc:*
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sp_rodent:*
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578
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773.9
733.9
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Perfect score:
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064487; 064486; 064488; 064495; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, D PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE DELTA) (R-PTP-DELTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takura H.;
"MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized regions of the brain and in the B-cell lineage.";
Mol. Cell. Biol. 13:5513-5523(1993).
                                                                                                                                                                                                                                                                                                                                                                         "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
"A novel receptor-type protein tyrosine phosphatase with a single catalytic domain is specifically expressed in mouse brain.";
Biochem. J. 305:499-504(1995).
-:- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + PHOSPHATE.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
MEDLINE-93360986; Pubmed-8355697;
Mizuno K., Hasegawa K., Katagiri T., Ogimoto M., Ichikawa T.,
                                                                                                                                                      Oliver K., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 AA; 46712 MW; 809E0091B7834D80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2;
Pred. No. 24;
1; Mismatches
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MEDLINE-95134232; PubMed-7832766;
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STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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EMBL; AL031182; CAA20169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                   Streptomyces coelicolor.
 PUTATIVE LIPOPROTEIN.
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                                                                                                                    SEQUENCE FROM N.A.
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31 GRLCVQP 37
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SEQUENCE 4
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MEDLINE=93119270; PubMed=8380322;
Honda M., Kaneko S., Unoura M., Kobayashi K., Murakami S.;
Sequence analysis of putative structural regions of hepatitis C virus isolated from 5 Japanese patients with hepatocellular carcinoma.";
Arch. Virol. 128:163:163:169(1993).
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Hepacivirus
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
(JK4) CORE, E1, NSI/E2 AND NS2 GENES (FRAGMENTS).
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Last annotation update)
                                                                                    PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
PROSITE; PS00280; BPTI_KUNITZ; UNKNOWN_1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; UNKNOWN_6.
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Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                            1; Mismatches
                                  PRINTS; PR00261; LDLRECEPTOR.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
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Pred. No.
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PFAM; PF00754; F5_F8_type_C; 1.
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75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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01-NOV-1998 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
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Gaps

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Length 447; Indels 236 AA.

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SEQUENCE FROM N.A.
STRAIN=CV. LEMONT;
Vysotskaia V.S., Schwartz J.R., Osborne B.I., Wing R., Yu G., Kwan A.,
Liu S., Lee J., Toriumi M., Luros J., Li J., Kremenetskaia I., Oji O.,
                                                                                                                             Oryza sativa (Rice).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                       "Oryza sativa chromosome 1 BAC 10A191.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AAC007858; AAD39593.1; ...
INTERPRO; IPRO10059; ...
SEQUENCE 236 AA; 26681 MW; 0A33BES977933E42 CRC64;
                                          U1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
10A191.8.
                                                                                                                                                                                                                                            Theologis A.;
"Oryza sativa chromosome 1 BAC 10A19I.
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Best Local Similarity 100.
Matches 6; Conservative
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SEQUENCE
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Q9L8F5;
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Q9L8F5
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Q9XHV8
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R MGD; MGI:97812; Ptprd.

R INTERPRO; IPR000242; ---

R INTERPRO; IPR000342; ---

R INTERPRO; IPR000377; ---

R INTERPRO; IPR001777; ---

R INTERPRO; IPR00141; Fai; 3.

R PFAM; PF00041; Fai; 3.

R PRAM; PF00041; Fai; 3.

R PRAM; PF000141; Fai; 3.

R PRINTS; PR000141; Fai; 1.

R PRINTS; PR00010; TYR_PHOFPHARASE_1; FALSE_NEG.

R PROSITE; PS000383; TYR_PHOSPHATASE_2; 4.

R PROSITE; PS500055; TYR_PHOSPHATASE_2; 4.

RW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Duplication; Minunoglobulin domain; Alternative splicing; Repeat.
-i- ALTERNATIVE PRODUCTS: AT LEAST THREE DIFFERENT ISOFORMS; TYPE A, B, AND C (SHOWN HERE); ARE DUE TO ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: BRAIN, KIDNEY, HEART, AND SOME B-CELL LINES.
-i- PTW: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN FROM THE TRANSMEMBRANE SEGNENT (BY SIMILARRITY).
-I- SIMILARITY: EXTRACELLULAR REGION TYPICAL OF A CAM FAMILY (3 IG-LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND EMBL; D13903; BAA03003.1; --
EMBL; D13905; BAA03005.1; --
EMBL; D13905; BAA03006.1; --
EMBL; Z23051; CAB0586.1; --
HSSP; P18952; IYPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND B ISOFORMS).
MISSING (IN TYPE A AND B ISOFORMS).
MISSING (IN TYPE A ISOFORM).
EQE -> QRS (IN TYPE A.SOFORM).
HILCPDICTLN -> ATYCVRTFALLYK (IN REF. 2).
K -> E (IN REF. 2).
VPS -> FIA (IN REF. 2).
TESORLH -> RVNKTCN (IN REF. 2).
TESORLH -> RVNKTCN (IN REF. 2).
THESORLH -> RVNKTCN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-
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M -> MCLTSCFILASHMLSCDLVFVP (IN TYPE A
                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FURNINGTIN TYPE-III.
FURNINGTIN TYPE-III.
FURNINGTIN TYPE-III.
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BY SIMILARITY.
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Gaps

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Indels

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Length 236;

DB 10; 32;

76.1%; Score 35; DB 100.0%; Pred. No. 32; Live 0; Mismatches

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MEDLING-20143766; PubMed-10678967;
Boyd E.F., Moyer K.E., Shi L., Waldor M.K.;
Boyd E.F., Moyer K.E., Shi L., Waldor M.K.;
Infectious CTXPhi and the vibrio pathogenicity island prophage in vibrio mimicus: evidence for recent horizontal transfer between V. mimicus and V. cholerae.";
Infect. Immun. 68:1507-1513(2000).
EMBL, AP207887; AR40142.1; -.
                                                                                                                                                  Vibrio mimicus.
Bacteria: Proteobacteria: gamma subdivision: Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 323
323 AA; 36306 MW; 01C12DAE9B873C3B CRC64;
                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2
Pred. No. 43;
1; Mismatches
  323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.1%;
75.0%;
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PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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240 GRLCVQDG 247
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                                                                                                        ZOT (FRAGMENT).
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Gaps

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Score 37; DB 11; Length 1894; Pred. No. 85; 1; Mismatches 0; Indels (

Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative

1 GRVCVQP 7 ||||:|| 1667 GRVCLQP 1673

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RESULT

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Q9W095
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MEDLINE-204068313; Pubmed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hicky E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamarhevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L. Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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"Vibrio cholerae nct-CTXphi whole genome, include rstR(RstR),
rstA(RstA), rstB(RstB), cep(Cep), orfU(OrfU), ace(Ace) and zot(2ot)
genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                    Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                         Shin H.J., Park Y.C., Kim Y.C.; "Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-0139-TOR OGAWA;
bli-Yong H., Weil-Jie Z., Xiang-Fu W.;
"Cloning and Expression of zot Gene from Vibrio cholerae.";
submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 AA; 44903 MW; 3C7424B758176774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
20NULAR OCCLUDENS TOXIN (ZONA OCCLUDENS TOXIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2;
Pred. No. 51;
1; Mismatches
                   399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                     PRT;
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EMBL, AF175708; AAD51358.1; -.

EMBL, AF123049; AAD2684.1; -.

EMBL, AE004224; AAF94615.1; -.

TIGR, VC1458; -.

SEQUENCE 399 AA: 44903 MW; 3
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75.08;
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09L706;
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
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                     PRELIMINARY;
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Best Local Similarity
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291 GRLCVQDG 298
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                                                                                                                                               ZOT OR VC1458.
Vibrio cholerae
                                                                                                                                                                                                          NCBI_TaxID-666;
                                                                                                                                                                                                                                                                            STRAIN-KNIH002;
                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.
                                             Q9R3V6;
                     09R3V6
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REC STRAIN—BERKELEX;

RA Adams N.D. Celligher S.E., Holf R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celligher S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celligher S.E., Holf B.W., Hoskins R.A., Galle R.F.,

Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Tandell M.D., Zhango Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeliffer B.D.,

RA Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Malklos G.L.G.,

Abrill J.F., Apbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Bonco P.V., Berman B.P., Bandari D., Bolshako S.,

RA Borkova D., Botchan M.R., Burke B. D., Brokstein P., Bichtler P.,

RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Pavenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Pavenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Pavenport L.B., Davies P.,

RA Glodek A., Gong F., Gorell J.H., Gu Z., Galan P., Harris M.,

RA Horsin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Wolfer C.D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.

Jalali M., Mulshina N.V., Mobarry C., Morris J., Moshrefi A.,

Rount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Moshrefi A.,

Randerle B.C., Siden Klamos I., Simpson M., Strong R., Sun B.,

Randers B.C., Siden Klamos I., Simpson M., Strong R., Sun S., She H.,

RA Hilams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q., Zheng L.,

RA Hilams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q., Sheng L.,

Randens R.A., Werez E.W., Rhong G.W., Wu W., Strong R.,

Randens R.A., Werez E.W., Rhong G., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                ;
                                                                                                                                                                          Length 399;
                                                                                                                                                                                                                                                1; Indels
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF220606; AAF22547.1; -. SEQUENCE 399 Aa; 44990 MM; CF6A3DBCC9E23EEI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9W095 PRELIMINARY; PRT; 578 AA.
O9W095; Q9W094;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
CG7995 PROTEIN.
                                                                                                                                                                              5;
                                                                                                                                                                          DB
51;
                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                              Score 35;
Pred. No.
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                                                                                                                                                                              76.1%;
75.0%;
                                                                                                                                                                                 Query Match 76.1
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             291 GRLCVQDG 298
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RESULT 10

Matches

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December 1993-90675; PubMed-8512576;
Cleutat A.M., Rosa J.P., Letourneur F., Poncz M., Rifat S.;
Cleutat A.M., Rosa J.P., Letourneur F., Poncz M., Rifat S.;
Cleutat A.M., Rosa J.P., Letourneur F., Poncz M., Rifat S.;
T. ** Comparative analysis of convadentive sequences for rat and mouse beta 3 integrins (GPIIA) with their human counterpart.*;
Blochem. Blophys. Res. Commun. 193:771-778(1993).
RIVERPRO; IPR001069; ...
RIVERPRO; IPR001069; ...
RIVERPRO; IPR003269; ...
RIVERPRO; IPR003269; ...
RIVERPRO; IPR003269; ...
RIVERPRO; IPR00321; EGF_1; UNKNOWN_2.
RRIVE; PR001186; INTEGRINB.
RROSITE; PS00021; EGF_1; UNKNOWN_1.
RROSITE; PS001186; INTEGRIN_BETA 3.
RROSITE; PS001186; EGF_2; UNKNOWN_1.
RROSITE; PS001186; EGF_2; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Rattus.
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                                                      SEQUENCE FROM N.A.

11 X.L., Ljungdahl L.G., Gollin D.J.;
Submitted (COT-1996) to the EMBL/GenBank/DDBJ databases.

1- CATALYIC ACTIVITY: FORMATE + NADP(+) = CO(2) + NADPH.

1- CATALYIC ACTIVITY: FORMATE + NADP(+) = CO(2) + NADPH.

1- CATALYIC ACTIVITY: FORMATE + NADP(+) = CO(2) + NADPH.

1- CATALYIC ACTIVITY: FORMATE + NADP(+) = CO(2) + NADPH.

1- CATALYIC ACTIVITY: FORMATE + NADP(+) = CORACTOR: SEEBNIUM: TWOSTEN: IRON.

1- TREAPRO: PRO01005;
1- TREAPRO: PRO01005;
1- TREAPRO: PRO01005;
1- TREAPRO: PRO01009;
1- TREAPRO: PR
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Last annotation update)
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85.7%; Pred. No. 85;
Live 0; Mismatches
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75057 MW;
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ses 6; Conserv
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nes 6; Conserv
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   NCBI_TaxID=1525;
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548 VCVQPG 553
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TRANSMEM
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Q9QW16;
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RP SEQUENCE FROM N.A.

MEDLINE=93290675; PubMed=8512576;

RA Cleutat A.M., Rosa J.P., Letourneur F., Poncz M., Rifat S.;

R1 "A comparative analysis of cDNA-derived sequences for rat and mouse peta 3 integrins (GPIIA) with their human counterpart.";

Biochem. Blophys. Res. Commun. 193:771-778(1993).

DR INTERPRO; IPR0010551, -..

DR INTERPRO; IPR002066; -..

DR INTERPRO; IPR002369; -..

DR INTERPRO; IPR002369; -..

DR PROSITE; PS00022; integrin_B; 1.

PRAM; PS00022; integrin_B; 1.

DR PROSITE; PS000243; INTEGRINB.

DR PROSITE; PS000243; INTEGRIN_BETRA; 3.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MusiCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group;
Moorella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
SUBUNIT (EC 1.2.1.43) (FORMATE
                                                                                                                                                                                                                                                                                                                           Length 578;
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                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                        h 76.1%; Score 35; DB Similarity 62.5%; Pred. No. 71; 5; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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EMBL; AE003472; AAF47559.1; -. HSSP; P08859; 1GLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQQW15
QQQW15;
Q1-MAY-2000 (TrEMBLrel. 13, Cx
Q1-MAY-2000 (TrEMBLrel. 13, La
Q1-JUN-2000 (TrEMBLrel. 14, La
BETA 3 INTEGRIN, GPIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P77907;
01-FEB-1997 (TrEMBLEEL 02, 01-FEB-1997 (TrEMBLEEL 02, 01-CT-2000 (TrEMBLEEL 15, FORMATE DEHYDROGENASE, BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
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286 GQMCVKPG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GRVCVQPG 8
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509 VCVQPG 514
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P77907

RESULT 11

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Matches

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142 GMVCVQP 148
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                                                                      Q59545
Q59545;
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                                               RESULT
Q59545
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STRAIN-GUILLARD (1991) CCMP 1203;
STRAIN-GUILLARD (1991) CCMP 1203;
MEDLINE-96177564; PubMed-8604305;
Cermakian N., Ikeda T.M., Cedergren R., Gray M.W.;
Cermakian N., Ikeda T.M., Cedergren R., Gray M.W.;
Sequences homologous to yeast mitochondrial and bacteriophage T3 and T7 RNA Polymerases are widespread throughout the eukaryotic lineage.";
Nucleic Acids Res. 24:648-654(1996).
EMBL; U34286; AAB01080.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                      Oresnik 1.J., Pacarynuk L.A., O'Brien S.A.P., Yost C.K., Hynes M.F.; "Plasmid Encoded Catabolic Genes in Rhizobium leguminosarum by. trifolil: Evidence for a plant inducible rhamnose locus involved in competition for nodulation."

EMBL, Plant Microb Interact. 0:0-0(1998).

EMBL, AF086782; AAD11983.1; -...

FINERRO, IPR001328; -...

PROSITE, PS00059; ADH_ZINC; 1.

Plasmid; Oxidoreductase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Pycnococcaceae; Mycnococcus. NCBI_TaxID-41880;
                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=386;
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Pred. No. 46;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                              Length 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24820 MW; 933F6D489F7B2FCD CRC64;
                                                                                                                                                                                                                                                                                                                                           96 AA; 10288 MW; D809EC6E706DFF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
13/T7-LIKE RNA POLYMERASE (FRAGMENT).
                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2
Pred. No. 22;
2; Mismatches
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                            96 AA.
                                                                                                            Rhizoblum leguminosarum (biovar trifolii).
Plasmid pRlew14-2c.
                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                 01-NOV-1998 (TrEMBLrel. 08, Created O1-NOV-1998 (TrEMBLrel. 08, Last st 01-NAY-2000 (TrEMBLrel. 13, Last at SORBITOL DEHYDROGENASE (FRAGMENT).
                            PRT;
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1 1 1 1 217

217 217 217

5 217 AA; 24820 MW; 9
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Best Local Similarity 85.7%;
Matches 6; Conservative
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pycnococcus provasolii.
                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-RLT100;
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87 RVCMEPG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RVCVQPG 8
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SEQUENCE
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SEQUENCE
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1 GRVCVQP 7

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 14, Last annotation update)
xYLITOL DEHYDROGENASE (EC 1.1.1.9) (D-XYLULOSE REDUCTASE).
MOGGABAELLA morganii (Proteus morganii).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                      Thesis (1991), University of Wisconsin-Madison, Madison, USA.
-!- CATALYTIC ACTIVITY: XYLITOL + NAD(+) = D-XYLULOSE + NADH.
EMBL: L34345; AAA25324.1;
HSSP: P07846; LSDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 338;
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Pred. No. 69;
2; Mismatches
338 AA
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 PRT;
                                                                                                                                                                                                                                                                                                                                                PFAM; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
milarity 71.4%;
Conservative 2
 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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RVCMEPG 92
                                                                                                                                                               NCBI_TaxID=582;
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Gaps

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TELECOMMUNICATION INFORMATION: TELEPHONE: (202)414-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SECTION OF 8: SEQUENCE CHARACTERISTICS: LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Vibrio cholerae
STRAIN: El Tor 7946
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              (202)414-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                       US-08-624-601-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-624-601-8
Appli
, Appl
                                                             (without alignments)
1.296 Million cell updates/sec
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Sequence 48,
                                                                                                                                                                                                                                                                                                                                                  Description
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Sequence 3
Sequence 2
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                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
      version 4.5
- 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                              US-08-486-399-24
US-08-461-965-24
US-08-326-110A-53
                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                        185757 seqs, 19210857 residues
                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     protein search, using sw model
                                                    June 13, 2001, 14:08:19
                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
      GenCore
Copyright (c) 1993
                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                PCT-US01-05825A-1
46
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                                                                                                  GRVCVQPG 8
                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                 Title:
Perfect score:
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Maximum DB
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                                                    Run on:
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No.
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## ALIGNMENTS

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OCTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,792
FILING DATE: 19-May-1995
CLASSIFICATION: 435
                                                                         COUNTRY: United States of America 2IP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380227
FILING DATE: 30-3AN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/08444792; Patent No. 5726037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.5
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-728-215-41
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                 CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                          Gaps
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Patent No. 5962643
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
TITLE OF INVENTION: A No. 43
                                                                                                                                                                                                                    Sequence 39, Application US/07728215
Patent No. 562643
Patent No. 562643
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Nobert
TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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DB 2; Length 400;
56;
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                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pretty, Schroeder, Brueggemann & Clark 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/728,215
FILING DATE: 19910711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB
Pred. No. 20;
1; Mismatches
                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICAL...
FILING DATE: 19910711
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNWBER: 31,815
TELECOWMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
; INPORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4370 La Jolla Villaye Lill.
CITY: San Diego
STATE: California
COUPTE: United States of America
ZIP: 921.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Score 35;
Pred. No.
76.1%;
Query Match 76.1
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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291 GRLCVQDG 298
                                                                               1 GRVCVQPG 8
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|82 VCIQPG 87
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APPLICANT: Gorman, Cornella M.
APPLICANT: McLean, John W.
APPLICANT: Mary A.
TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                               COMPUTER KEADABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/728,215
FILING DATE: 19910/711
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEG ID NO: 41:
SEQUENCE CHARACTERISTICS:
LLENGTH: 92 amino acids
E: Pretty, Schroeder, Brueggemann & Clark
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Generatech, Inc.
STREET: Geo. Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
COUNTRY: USA
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GENERAL INFORMATION:
APPLICANT: Sheppard, Vito
APPLICANT: Pytela, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 91122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 718;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/728,215
FILING DATE: 19910711
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RESISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
WUNDER ANTON ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                           P0552P1C3D1
                           APPLICATION NUMBER: 07/44490
FILING DATE: 01-DEC-1989
PRIOR APPLICATION DATA:
PILING DATE: 22-DEC-1988
ATORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
TELECOMMUNICATION INFORMATION:
TELECHONE: 415/25-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/07728215 Patent No. 5962643
                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.9
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 VCIQPG 618
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APPLICANT: Bodary, Sarah C.
APPLICANT: Gorman, Cornelia M.
APPLICANT: McLean, John W.
APPLICANT: McLean, John W.
TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE:
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: 461 Foint San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 718;
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               P0552P1C3D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,042
CLASSIFCATION: 530
APPLICATION NUMBER: 08/218878
FILING DATE: 28-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/82137
FILING DATE: 13-JAN-1992
PRIOR APPLICATION DATA: 07/44490
FILING DATE: 01-DEC-1989
PRIOR APPLICATION DATA: 07/44490
FILING DATE: 22-DEC-1989
PRIOR APPLICATION NUMBER: 07/29024
FILING DATE: 22-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380227
FILING DATE: 30-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/218878
FILING DATE: 28-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821337
FILING DATE: 13-JAN-1992
                                                                                                                                                                                                                                                             NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1994
TELEX: 910/31/-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08445042
Patent No. 5726290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.98;
83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 718 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-445-042-4
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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twonsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUMTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING DATE: 19-NOV-199/
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643

FILLING DATE: 01-0CT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILLING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILLING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050

FILLING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-0CT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-0CT-1997

PRIOR APPLICATION NUMBER: 36,429

REGESTRATION NUMBER: 36,429

REFERENCE/POCKET NUMBER: 36,429

REFERENCE/POCKET NUMBER: 36,429

REFERENCE/POCKET NUMBER: 36,429
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                                                                                                                                                                                                                                                                 ; Sequence 324, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
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49 GRLCAGPG 56
1 GRVCVQPG
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                                       Score 34; DB 2; Length 788;
Pred. No. 1.6e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Twomsend and Townsend and Crew LLP
STREET: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
STRTE: California
COUNTRY: United States of America
ZIP: 94111 united States of America
ZIP: 94111 EMPCOMPATISH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
RECESTRATION NUMBER: 36,420
RELECOMMUNICATION NUMBER: 36,63000
FINDEMATION FOR SEC ID NO: 205:
COUNTY: NEW PROMATION:
NAME: APPLICATION FOR SEC ID NO: 205:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 205, Application US/08851843A Patent No. 6093809 GENERAL INFORMATION:
                                               Query Match 73.9%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 76 amino acids amino acids
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Matches 5; Conservative
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| 613 VCIQPG 618
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US-08-445-135-2
Sequence 2, Application US/08445135
Sequence 2, Application US/08445135
Sequence 2, Application
Sequence 2, Application
Sequence 3, Application
GENERAL INFORMATION:
APPLICANT: QUaranta, Vito
APPLICANT: Horman, Marketta
TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CANT
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                                                                                                                                                                                                                           DB 2; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER FALORE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILE
COMPUTER: IBM PC COMPAILE
COMPUTER: DATE:
COMPUTER: PACHOLIN BC-
SOFTWARE: PACHOLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,135
FILING DATE:
CLASSIFICATION: 435
PRICK APPLICATION 1048ER: US/08/151,134
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: DESMOS.002CP2
TELECOMMUNICATION: NUMBER: DESMOS.002CP2
TELECOMMUNICATION: NUMBER: DATE.
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                           Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 235-8850
TELEFAX: (619) 235-8850
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                           69.68;
75.08;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                            SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-12
                                                                                                                                                                                                                        Query Match 69.6
Best Local Similarity 75.0
Matches 6; Conservative
     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRAGMENT TYPE: 1:
; IMMEDIATE SOURCE:
; CLONE: 150 kD
US-08-445-135-2
                                                                                                                                                                                                                                                                                                                                                                                         8 GRALVQPG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                   1 GRVCVQPG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08652816A
Patent No. 5872153
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Mccafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDIRESEE: MATSHAIL, O'TOOLE, GETSTEIN, MILTAY & BOLUN STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STRET: 1111nois COUNTRY: United States of America COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: Ploppy disk COMPUTER: D'EACHING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: PSPLICATION NAME: D3-MAY-1996 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NAMER: GB 9206318.9 FILING DATE: 24-MAY-1992 PRIOR APPLICATION NAMER: GB 9206312.6 FILING DATE: APPLICATION DATA: APPLICATION NAMER: GB 9206372.6 FILING DATE: APPLICATION NAMER: GB 9206372.6 FILING DATE: APPLICATION NAMER: GB 9206372.6 FILING DATE: APPLICATION DATA: APPLICATION NAMER: GB 9206372.6 FILING DATE: APPLICATION NAMER: GB 9206372.6 FILING DATE: APPLICATION NAMER: GB 9206372.6 FILING DATE: O'-DEC-1992 PRIOR APPLICATION NAMER: GB 9206372.7 FILING DATE: D3-MAY-1996 PILING DATE: O'-DEC-1992 PILING DATE: O'-DEC-1993 PILING DATE: O'-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                  DB 4; Length 76;
37;
                                                                                                                                                                                                                                               Score 32; DB 4
Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                               69.6%;
62.5%;
                         ; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLGGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-324
                                                                                                                                                                                                                                            Query Match 69.6
Best Local Similarity 62.5
Matches 5; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                              49 GRLCAGPG 56
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US-08-652-816A-12
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APPLICANT: YVES R. LAIOCHE, LAUTENT S. JESPEIS,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: LVOOR STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Goorge P. Lancele, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Year R. Laroche, Laurent S. Jespers,
APPLICANT: Year B. Bergum
TITLE OF INVENTION: NEMATOR-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 2;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
APTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANTE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
FELECOMMUNICATION INFORMATION:
THERCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. DOS 5.0
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los and
                                                                                                                                                                                                                                           E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                   90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-486-399-48
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                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                               APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
WUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: George P. Vlasuk, Patric H. Stanssens. APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSTRICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancyclostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
(213) 489-1600
LELERAX: (213) 955-0440
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08486397
Patent No. 5865542
GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 48, Application US/08465380 Patent No. 5863894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 RVCFRPG 54
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560 VCLQPG 565
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US-08-465-380-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-486-397-48
                                                                                                                                                                                                    US-08-465-380-48
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...crLCANT: Lauvereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
ADDRESSED ADDRESS:
ADDRESSEE: Lvor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/634,641
FILING DATE: April 19, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCCODER 17, 1995
APPLICATION NUMBER: PCT/CS95/13231
APPLICATION NUMBER: PCT/CS95/13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.4%; Score 31; 71.4%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 06/cbber 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS. SUZANNE L.
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELEFHONE: (213) 489-1600
TELEFA: 67-3510
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Ancyclostoma ceylanicum
US-08-461-965-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08634641
Patent No. 5955294
GENERL INFORMATION:
APPLICANT: Vlasuk, George P. Vla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
    June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | : | |
48 RVCFRPG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RVCVQPG 8
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US-08-634-641-48
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Sequence 48 Application US/08461965

Sequence 48 Application US/08461965

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Application:

APPLICANT: Yeas R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,

APPLICANT: Peter W. Berguum

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 89;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB
Pred. No. 64;
1; Mismatches
                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: IEM COMPATIBLE OPERATING SYSTEM: IEM COMPATIBLE OPERATING SYSTEM: IEM P.C. DOS 5.0 SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/486,399 FILING DATE: June 5, 1995 CLASSIFCATION NUMBER: 08/326,110 APPLICATION NUMBER: 08/326,110 APTCRNEY AGENT INFORMATION: NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 213/270 TELECOMUNICATION INFORMATION: TELECOMUNICATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancyclostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/461,965
                                                                                                                                                                                                                                                                                                                                                                                                                                           : LLEFAX: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:\
LENGTH: 89 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                    U.S.A.
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48 RVCFRPG 54
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US-08-486-399-48
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Query Match 67.4%; Score 31; DB 2; Length 89; Best Local Similarity 71.4%; Pred. No. 64; Matches 5; Conservative 1; Mismatches 1; Indels
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08,461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
ATORNEY/AGENT INFORMATION:
NAME: BIGGS. SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECOMUNICATION INFORMATION:
TELECHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-310
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: Almear
NOLECULE TYPE: peptide
ORIGINAL SOURCE:
CREANISM: Ancyclostoma ceylanicum
US-08-634-641-48
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0; Gaps

Search completed: June 13, 2001, 14:16:31 Job time: 492 sec

2 RVCVQPG 8 ||| :|| 48 RVCFRPG 54

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Human zona pelluci Human oocyte zona Human zona pelluci Human zona pelluci PTPase PTP35 #2.

Rhotekin, bi Rhotekin pro zona pelluci

Mouse Human

Am1.no Human Human Human Human Нишап

correlat

zona pelluci zona pelluci ZPA protein.

Mature nematode ex Human ORFX ORF237 Mature nematode ex A. caninum nematod

Breast and ovarian A human cancer-ass Amino acid sequenc

Peptide antagonist

PTPase PTP35 #2. Kuman islet cell

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Amino acid

Peptide antagonist Peptide antagonist Peptide antagonist

Human secreted pro Soybean vestitone Soybean vestitone

New peptide antagonist of zonulin useful as antiinflammatory agent for

WPI; 2000-205565/18

782 785

Score

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Result

Human secreted pro Sugar transferase AcaNAP47. Ancylos Nematode extracted

Perfect score:

Title:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Database :

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blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic; gastrointestinal inflammation; therapy.
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                                                                                                                                                                                                             X37051
Y79113
Y79117
Y79126
Y30424
B40473
                                                                                                                                                                                                                                                                                                                             W75215
W88312
B65019
Y05529
         Y44560
B26790
W28865
Y44559
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R49039
Y06606
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Y35642
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B07747
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R91712
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                                                       R74094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y79106 standard; Peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide antagonist of zonulin.
98US-0127815
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228
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465
949
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97
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162
181
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Fasano A;
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RESULT
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Peptide antagonist
Peptide antagonist
Peptide antagonist
Peptide antagonist
Peptide antagonist
Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide antagonist
Peptide antagonist
Zonula occludens t
                                                                        ; Search time 229.28 Seconds
(without alignments)
1.995 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                   | Single Seggdata/geneseqp/Aa1980.DAT:*
| Single Siggdata/geneseqp/Aa1981.DAT:*
| Single Siggdata/geneseqp/Aa1981.DAT:*
| Single Siggdata/geneseqp/Aa1981.DAT:*
| Single Siggdata/geneseqp/Aa1981.DAT:*
| Single Siggdata/geneseqp/Aa1984.DAT:*
| Single Siggdata/geneseqp/Aa1984.DAT:*
| Single Siggdata/geneseqp/Aa1984.DAT:*
| Single Siggdata/geneseqp/Aa1987.DAT:*
| Single Siggdata/geneseqp/geneseqp/Aa1997.DAT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                    390729 segs, 57163235 residues
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Listing first 45 summaries
                                                      protein search, using sw model
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Y79110
R20006
X79105
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Match
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93.3
93.3
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84
84
77
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WPI; 2000-205565/18.

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This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (207) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor. Uniding. They can be prepared by chemical synthesis or by use of antinflammatory agents. The peptide antagonists are used as an antinflammatory agents in the treatment of gastrointestinal antisetine. Gastrointestinal inflammation, where they bind to the ZOT receptor in the intestine increased intestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite minestino, bacterial lovergrowth, whipple's disease, diseases with
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphangiectasia, sarcoidosis lymphangiectasia, correction of congenital heart disease with Fontan's operation of congenital heart disease with Fontan's operation, correction of congenital correction, e.g. Menetrier's disease, coellac disease, eosinophilic gastroenteritis, and immune diseases,
                   meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g. systemic lupus erythematosus or food allergies, primarily to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 45; DB 21; Length 8; 100.0%; Pred. No. 3.2e+05; Live 0; Mismatches 0; Indels
cerebral edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal inflammation; therapy
  treating cerebral ischemia, stroke, shigellosis, viral gastroenteritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV MARYLAND BALTIMORE.
                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y79110 standard; Peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 8; Conservative
                                                             Claim 1; Page 41; 69pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GRVCVQDG 8
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                                                                   New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           caused by infection, e.g. Clostridium difficile infection, enterocolitis, shigellosis, viral gastroenteritis, parasite infestation, bacterial overgrowth, whitple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous colitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphanglectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mucosal diseases without ulceration, e.g. Menetrier's disease, coeliac disease, eosinophilic gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to milk.
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                                                                                                                                                       English.
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                       Claim 1; Page 42; 69pp;
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| grlcvqdg 8
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R20006
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physiologically modulate the opening of mammalian tight junctions and human zonulias, which is believed to a common motif of 20T and human zonulias, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an atinifiammatory agents. In the treatment of gastrointestinal inflammation, where they bind to the 20T receptor in the intestine and yet does not physiologically modulate the opening of TJ in the increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, e.g. clostridium difficile infection, caused by infection, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous collitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphanglectasia, sarcoidosis lympham, mesentic tuberculosis, and after surgical moreral disease with Fontan's ordered heart disease with formatory and after surgical correction of congenital heart disease with Fontan's ordered disease marked by correction of congental heart disease with Fontan's ordered in mesented tuberculosis, and after surgical moreral disease with formatory and after surgical disease with formatory and after s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                       coeliac disease, eosinophilic gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to milk.
                                                                                                                                                                                                                                                                                                                                                                                                 diseases without ulceration, e.g. Menetrier's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic; gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 8;
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Pred. No. 3.2e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5.
Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   mucosal diseases
coeliac disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA;
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                                                                                                                                                                                                                             It may be responsible for diarrhoea in some strains of cholera and the 20T gene or fragments of it are deleted from strains of vibrio-cholerae (V.c.) to be used as vaccines. These V.c. strains have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodn. of vaccines against cholera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                          The amino acid sequence is that of the zonula occludens toxin (20T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This present sequence is that of a peptide antagonist of zonulin (2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (20T) receptor, yet do not
                                                                                                     New Vibrio cholerae strains - comprise restriction endonuclease fragment encoding toxin, used as vaccines against cholera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
Pred. No. 5
                                                                                                                                                                   Disclosure; Fig 18; 83pp; English.
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    Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%;
87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
                                           1992-007465/01
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                                                              N-PSDB; Q20185.
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    Kaper JB,
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28-JUL-1999;
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                  This present sequence is that of a peptide antagonist of zonulin (27), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (207) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT combinant zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an tinflammation, where they bind to the ZOT receptor in the intestina inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the case of the starointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal permeability and the peptide is useful for caused by infection, e.g. clostridum difficile infection, e.g. congenital intestinal lymphaniectasia, lymphatic obstruction, e.g. congenital intestinal lymphaniectasia, mescenteric tuberculosis, and affers surgical correction of congenital heart disease, and immune disease, conformation, e.g. wenetrier's disease, eccinosis and interview or inferience or reformation, e.g. meinteritis, and immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                e.g. systemic lupus erythematosus or food allergies, primarily to
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 8;
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0; Mismatches 1; Indels
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   Claim 1; Page 44; 69pp; English
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Best Local Similarity 87.5
France 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         8 AA;
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(2), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (207) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (7J). The peptide antagonists are based on a common motif of 207 and human zonulins, which is believed to be critical for receptor in formation. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an inflammation, where they bind to the 207 receptor in the intestine and yet does not physiologically modulate the opening of TJ in the intestine. Gastrointestinal inflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, caused by infection, e.g. Clostridium difficile infection, caused by infection, e.g. Clostridium difficile infection, micestation, bacterial overgrowth, whipple's disease, diseases with micosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous collits, inflammatory bowel disease, disease marked by
New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphatic obstruction, e.g. congenital intestinal lymphanglectasia, sarcoidosis lymphoma, mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, mucosal diseases without ulceration, e.g. Menetrier's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coeliac disease, eosinophilic gastroentéritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to
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Pred. No. 3.2e+05;
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                                                                                                                                                                                     Claim 1; Page 45; 69pp; English
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87.5%;
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Matches 7; Conserv
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99WO-US16683

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28-JUL-1999;
                                                                                                Fasano A;
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                                                                                                                                                        This present sequence is that of a peptide antagonist of zonulin (27), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (207) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an inflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the and yet does not physiologically modulate the opening of TJ in the and yet does not physiologically modulate the opening of TJ in the cased intestinal permeability and the peptide is useful for intestine. Gastrointestinal inflammation conditions give rise to increased intestinal conditions that cause protein losing enteropathy enterotion, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, parasiste infection, bacterial overgrowth, whipple's disease, diseases marked by impatic obstruction, e.g. coopenital intestinal lymphaniectasia, sarcoidosis lymphanie mesenteric tuberculosis, and after surgical correction of congenital heart disease with Fontan's operation, mucosal disease, eosinophilic gastroenteritis, and immune disease, ceg, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                               New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 21; Length 8; Pred. No. 3.2e+05; 0; Mismatches 1; Indels
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                                                                                                                                     Claim 1; Page 42; 69pp; English.
(UYMA-) UNIV MARYLAND BALTIMORE
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                                                     WPI; 2000-205565/18
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Matches 7; Conserv
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| grvlvqdg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                             Fasano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x79109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Y79109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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This present sequence is that of a peptide antagonist of zonulin (12), one of 25 such peptides (see Y79105-29) of the invention, which blud to a zonula occludens toxin (207) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of Zon and human zonulins, which is believed to be critical for receptor binding. They can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an inflammation, where they bind to the Zon receptor in the intestine and yet does not physiologically modulate the opening of TJ in the cansed intestinal enflammation conditions give rise to increased intestinal permeability and the peptide is useful for treating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficile infection, caused by infection, e.g. Clostridium difficile infection, mocosal erosion or ulcerations, e.g. quastritis, gastric cancer, collagenous collits, inflammatory bowel disease, diseases marked by impatic obstruction, e.g. congenital intestinal lymphanictasia, arreading interation, asserted to congenital intestinal lymphanictasia, arreading interaction, asserted to congenital intestinal lymphanictal arreading arreading interaction, asserted tuberculosis, and after surgical correction of congenital heart disease with Fontant of congenital heart disease diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mucosal diseases without ulceration, e.g. Menetrier's disease, coellac disease, eosinophilic gastroenteritis, and immune diseases, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                                                                                                                                                                                                                                                                    New peptide antagonist of zonulin useful as antiinflammatory ageni
treating cerebral ischemia, stroke, cerebral edema, gastritis,
shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     blood-brain barrier; antiinflammatory; cerebroprotective; neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antiallergic; hypotensive; immunosuppressive; antiparasitic; vasotropic; gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 21; Length 8; Pred. No. 3.2e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zonulin; antagonist; zonula occludens toxin receptor;
                                                                                       (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 42; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y79122 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide antagonist of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.8%; 75.0%;
98US-0127815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                            WPI; 2000-205565/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1 GRVCVQDG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1998;
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haematopoiesis regulation; tissue growth; haemostasis; inflammation.

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                                                                                                                                                                                                                                                                                                                                                                                                                     This present sequence is that of a peptide antagonist of zonulin (z), one of 25 such peptides (see Y79105-29) of the invention, which bind to a zonula occludens toxin (ZCT) receptor, yet do not physiologically modulate the opening of mammalian tight junctions (TJ). The peptide antagonists are based on a common motif of ZOT and human zonulins, which is believed to be critical for receptor in they can be prepared by chemical synthesis or by use of recombinant DNA techniques. The peptide antagonists are used as an inflammation, where they bind to the ZOT receptor in the intestine antinflammation, where they bind to the ZOT receptor in the intestine and yet does not physiologically modulate the opening of TJ in the increased intestinal permeability and the peptide is useful for creating intestinal conditions that cause protein losing enteropathy caused by infection, e.g. Clostridium difficibe infection, caused by infection, e.g. clostridium difficibe infection, caused by infection, e.g. clostridium difficibe infection, cancer, infestation, bacterial overgrowth, whipple's disease, diseases with mucosal erosion or ulcerations, e.g. gastritis, gastric cancer, collagenous collitis, inflammatory bowel disease, diseases marked by lymphatic obstruction, e.g. congenital intestinal lymphanglectasia, sarcoldosis lymphan, mesenteric tuberculosis, and after surgical correction of congenital heart disease, disease, disease, disease, coslinghilic gastroenteritis, and immune disease, coslinghilic gastroenteritis, and immune disease, e.g. systemic lupus erythematosus or food allergies, primarily to
                                                                                                                                                                                                                                                                                                           agent for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                           New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 21; Length 8;
Pred. No. 3.2e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein SEQ ID NO: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B23609 standard; Protein; 782 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 46; 69pp; English.
                                                                                                                                                                                            (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.8%;
75.0%;
                                                                                                                99WO-US16683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GRVCVQDG 8
                                   WO200007609-A1.
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| gglcvqdg
                                                                                                                28-JUL-1999;
                                                                           17-FEB-2000
Synthetic.
                                                                                                                                                                                                                                      Fasano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B23609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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The present sequence is the sequence of a human secreted protein. Its CDNA was isolated from an adult brain cDNA ilbrary. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                   New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.6%; Score 34; DB 21; Length 782; 85.7%; Pred. No. 2.8e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                  Rapiejko P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein; cytokine; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                   Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page 250-253; 309pp; English
                                                                10..22
/label= signal_peptide
23..782
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SEQ ID NO: 92.
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B23636 standard; Protein; 785 AA.
                                                                                                                                                                                                                                                       99US-0155686.
99US-0157247.
99US-0167822.
                                                                                                                                                                                       18-FEB-2000; 2000WO-US04340.
                                                                                                                                                                                                                   99US-0120680
                                                                                                                                                                                                                                99US-0298733
99US-0149639
                                                                                                                                                                                                                                                                                                99US-0167823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85./.
                                                                                                                                                                                                                                                                                                                                                                     Valenzuela D, .Yuan O,
                                                                                                                                                                                                                                                                                                                                         (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-549267/50.
N-PSDB; A93109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 grvcvnd 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GRVCVQD 7
                                                                                                                                   WO200049134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-2001
                                                                                                                                                                                                                                23-APR-1999;
17-AUG-1999;
23-SEP-1999;
                          Homo sapiens
                                                                                                                                                                                                                                                                                      29-NOV-1999
                                                                                                                                                                                                                                                                                                     29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B23636;
                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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(GEST ) GENSET
                                                                                             28-NOV-1997;
17-DEC-1997;
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              WO9928475-A2
                                                           27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saptens
                                                                                04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2000
                                                                                                                                                    Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Y44560
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                     The present invention is concerned with a number of secreted proteins and their coding sequences isolated from various human cDNA libraries. The proteins and coding sequences can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as immurfathonal supplements, as cytckine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoissis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotractic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity, No information about sequences B23632-B23645 is given in the specification.
                                                                                                                                                                                                                                                                                                     New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 21; Length 785;
Pred. No. 2.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                          Rapiejko P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                         Hoffman H, Hall J,
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 298-300; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y36831 standard; Protein; 196 AA.
                                                                                                                         99US-0120680.
99US-0298733.
99US-0149639.
99US-0155686.
99US-0157247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.68;
                                                                                                     2000WO-US04340
                                                                                                                                                                                                99US-0167823
                                                                                                                                                                                                          15-FEB-2000; 2000US-0298733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                         Yuan O,
                                                                                                                                                                                                                                  (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis
                                                                                                                                                                                                                                                                              WPI; 2000-549267/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            785 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 grvcvnd 276
                                                       WO200049134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GRVCVQD 7
                                                                                                                                                                                                                                                         Valenzuela D,
                                  Homo sapiens.
                                                                                                     18-FEB-2000;
                                                                                                                                                 17-AUG-1999;
23-SEP-1999;
01-OCT-1999;
29-NOV-1999;
                                                                                                                            19-FEB-1999;
23-APR-1999;
                                                                              24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhotekin; Rho effector; Chromosome 2; target; GTP-activated Rho protein; susceptibility locus; Parkinson's disease; cytostatic; cardiant; primer; vaccine; probe; treat; cancer; cardiovascular disorder; brain disorder; developmental disorder; cytoskeletal-associated disorder; variant; EST; expressed sequence tag; signal transduction related disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 33; DB 20; Length 19
75.0%; Pred. No. 1.1e+02;
:1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 710-711; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y44560 standard; Protein; 527 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC
98WO-IB01939
                                                                                                   97FR-0015041.
                                                            98US-0107077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
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W28865
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                                                                                                                                                                                                                              The present amino acid sequence is the human Rhotekin variant protein, a putative target for Rho. It is derived from an EST and has close homology to Rhotekin polypeptide. It is a member of the Rho effector protein family and is located on chromosome 2, that has a susceptibility locus for Parkinson's disease. Rhotekin protein binds specifically to GTP-activated Rho proteins and interacts with downstream components of Rho-dependent signalling pathways. It has cytostatic and cardiant activity. This sequence may be used to identify agonists, antagonists or inhibitors and detect diseases associated with Rhotekin. The DNA sequence is useful as a source of primers and probes, while the proteins may be used as vaccines. Rhotekin sequences are used to treat diseases, such as acmore, cardiovascular diseases, brain disorders, developmental calated diseases.
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                                                                                                                            Gaps
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Pred. No. 2.9e+02;
L; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                      Calmels TPG;
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N-PSDB; Z29899.
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                      Duecker KN,
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using the polynucleotide. The polypeptide is a human Ras-related GTP binding kinase. The present sequence represents the protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein designated Rhotekin which binds Rho protein - useful to inhibit or treat tumour formation and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on; metastasis; antitumour; Rho binding protein; platelet aggregation; inflammation; gene therapy
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                                                                                                                                                             Score 33; DB 21; Length 544;
Pred. No. 2.9e+02;
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/label- Rho_binding_site
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Best Local Similarity 71.4%;
Matches 5; Conservative
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N-PSDB; T86255.
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Binding-site
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